

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
22 March 2001 (22.03.2001)

PCT

(10) International Publication Number  
WO 01/19988 A1

(51) International Patent Classification: C12N 15/12, C07K 14/47, C12N 1/21, 5/10, C12Q 1/68, A61K 38/17

(74) Agents: CARROLL, Alice, O. et al.; Hamilton, Brook, Smith & Reynolds, P.C., Two Militia Drive, Lexington, MA 02421 (US).

(21) International Application Number: PCT/US00/25135

(22) International Filing Date:  
14 September 2000 (14.09.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
09/398,829 17 September 1999 (17.09.1999) US

(71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02149 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

- With international search report.
- Before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments.
- With (an) indication(s) in relation to deposited biological material furnished under Rule 13bis separately from the description.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 01/19988 A1

(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract: Novel polynucleotides and the proteins encoded thereby are disclosed.

## 5 SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The  
10 now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as  
15 signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides  
20 encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AX65\_22 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;



(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AX65\_22 deposited with the ATCC under accession number 98196;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:1.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565; the nucleotide sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565; the nucleotide sequence of the full-length protein coding sequence of clone AX65\_22 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone AX65\_22 deposited with the ATCC under accession  
25 number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably  
30 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
35 NO:1 and SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X

5 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:1;

(ab) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

10 (ac) the nucleotide sequence of the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

15 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:1;

(bb) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bc) the nucleotide sequence of the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;

25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
30 sequence corresponding to the cDNA sequences of SEQ ID NO:1 and SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
35 NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:2;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising
- 25 a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD335\_14 deposited with the ATCC under accession number 98196;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD335\_14 deposited with the ATCC under accession number 98196;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:5;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:5;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:4.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318; the nucleotide sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825; the nucleotide sequence of the full-length protein coding sequence of clone BD335\_14 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BD335\_14 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:5 from amino acid 148 to amino acid 240. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid
- 30
- 35

sequence of SEQ ID NO:5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:5, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment comprising the amino acid sequence from amino acid 349 to amino acid 358 of SEQ ID NO:5.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:4.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 15 (aa) SEQ ID NO:4, but excluding the poly(A) tail at the 3' end of SEQ ID NO:4; and
    - (ab) the nucleotide sequence of the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - 25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:4, but excluding the poly(A) tail at the 3' end of SEQ ID NO:4; and
    - (bb) the nucleotide sequence of the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;
    - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
    - (iii) amplifying human DNA sequences; and
    - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:4, and extending contiguously from

a nucleotide sequence corresponding to the 5' end of SEQ ID NO:4 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:4, but excluding the poly(A) tail at the 3' end of SEQ ID NO:4. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:5;
- (b) the amino acid sequence of SEQ ID NO:5 from amino acid 148 to amino acid 240;
- (c) a fragment of the amino acid sequence of SEQ ID NO:5, the fragment comprising eight contiguous amino acids of SEQ ID NO:5; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:5 or the amino acid sequence of SEQ ID NO:5 from amino acid 148 to amino acid 240. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:5, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment comprising the amino acid sequence from amino acid 349 to amino acid 358 of SEQ ID NO:5.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG241\_1 deposited with the ATCC under accession number 98196;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG241\_1 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG241\_1 deposited with the ATCC under accession number 98196;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG241\_1 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight  
15 contiguous amino acids of SEQ ID NO:8;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:7.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391; the nucleotide sequence of the full-length protein coding sequence of clone BG241\_1 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BG241\_1 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide  
30 encodes the full-length or a mature protein encoded by the cDNA insert of clone BG241\_1 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ  
35 ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7, SEQ ID NO:6, and SEQ ID NO:9.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X  
10 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:6;

(ab) SEQ ID NO:7;

(ac) SEQ ID NO:9, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:9; and

15 (ad) the nucleotide sequence of the cDNA insert of clone  
BG241\_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in  
6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
consisting of:

25 (ba) SEQ ID NO:6;

(bb) SEQ ID NO:7;

(bc) SEQ ID NO:9, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:9; and

(bd) the nucleotide sequence of the cDNA insert of clone  
30 BG241\_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).



Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:6, SEQ ID NO:7, and SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:6 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BG241\_1 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762;

- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BL187\_4 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BL187\_4 deposited with the ATCC under accession number 98196;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:11;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:11;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:10.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762; the nucleotide sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762; the nucleotide sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050; the nucleotide sequence of the full-length protein coding sequence of clone BL187\_4 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BL187\_4 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention

provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:11, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:11.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:10.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:10, but excluding the poly(A) tail at the 3' end of SEQ ID NO:10; and

(ab) the nucleotide sequence of the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:10, but excluding the poly(A) tail at the 3' end of SEQ ID NO:10; and

(bb) the nucleotide sequence of the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:10 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:10, but excluding the poly(A) tail at the 3' end of SEQ ID NO:10. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:11;
- (b) a fragment of the amino acid sequence of SEQ ID NO:11, the fragment comprising eight contiguous amino acids of SEQ ID NO:11; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:11. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:11, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:11.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12  
5 from nucleotide 2 to nucleotide 2290;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12  
from nucleotide 134 to nucleotide 2290;
  - (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12  
from nucleotide 1 to nucleotide 309;
  - 10 (e) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone BL249\_18 deposited with the ATCC under accession  
number 98196;
  - (f) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone BL249\_18 deposited with the ATCC under accession number 98196;
  - 15 (g) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone BL249\_18 deposited with the ATCC under accession number  
98196;
  - (h) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone BL249\_18 deposited with the ATCC under accession number 98196;
  - 20 (i) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:13;
  - (j) a polynucleotide encoding a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:13 having biological activity, the fragment comprising eight  
contiguous amino acids of SEQ ID NO:13;
  - 25 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)  
above;
  - (l) a polynucleotide which encodes a species homologue of the protein of (i)  
or (j) above ;
  - (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(j); and
  - (n) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the  
length of SEQ ID NO:12.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:12  
35 from nucleotide 2 to nucleotide 2290; the nucleotide sequence of SEQ ID NO:12 from nucleotide

134 to nucleotide 2290; the nucleotide sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309; the nucleotide sequence of the full-length protein coding sequence of clone BL249\_18 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BL249\_18 deposited with the ATCC under  
5 accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID  
10 NO:13 from amino acid 3 to amino acid 102. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:13, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID  
15 NO:13 having biological activity, the fragment comprising the amino acid sequence from amino acid 376 to amino acid 385 of SEQ ID NO:13.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:12.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 25 (aa) SEQ ID NO:12, but excluding the poly(A) tail at the 3' end of SEQ ID NO:12; and
- (ab) the nucleotide sequence of the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
35 consisting of:

(ba) SEQ ID NO:12, but excluding the poly(A) tail at the 3' end of SEQ ID NO:12; and

(bb) the nucleotide sequence of the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:12, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:12 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:12, but excluding the poly(A) tail at the 3' end of SEQ ID NO:12. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:12 from nucleotide 15 2 to nucleotide 2290, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:12 from nucleotide 2 to nucleotide 2290, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:12 from nucleotide 2 to nucleotide 2290. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:12 from nucleotide 134 to nucleotide 2290, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:12 from nucleotide 134 to nucleotide 2290, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:12 from nucleotide 134 to nucleotide 2290. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:13;

(b) the amino acid sequence of SEQ ID NO:13 from amino acid 3 to amino acid 102;

35 (c) a fragment of the amino acid sequence of SEQ ID NO:13, the fragment comprising eight contiguous amino acids of SEQ ID NO:13; and

(d) the amino acid sequence encoded by the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:13 or the amino acid sequence of SEQ ID NO:13 from amino acid 3 to amino acid 102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:13, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment comprising the amino acid sequence from amino acid 376 to amino acid 385 of SEQ ID NO:13.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO71\_1 deposited with the ATCC under accession number 98196;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO71\_1 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;



(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:15.

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539; the nucleotide sequence of the full-length protein coding sequence of clone BO71\_1 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BO71\_1 deposited with the  
10 ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably  
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 8 to amino acid 17 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
20 NO:15, SEQ ID NO:14, and SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X  
25 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:14;

(ab) SEQ ID NO:15;

(ac) SEQ ID NO:17, but excluding the poly(A) tail at the 3'  
30 end of SEQ ID NO:17; and

(ad) the nucleotide sequence of the cDNA insert of clone  
BO71\_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);  
35

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in  
5 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
consisting of:

(ba) SEQ ID NO:14;

(bb) SEQ ID NO:15;

(bc) SEQ ID NO:17, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:17; and

10 (bd) the nucleotide sequence of the cDNA insert of clone  
BO71\_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
sequence corresponding to the cDNA sequences of SEQ ID NO:14, SEQ ID NO:15, and SEQ ID  
NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
SEQ ID NO:14 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide  
isolated according to the above process comprises a nucleotide sequence corresponding to the  
cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence  
corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end  
of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process  
25 comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from  
nucleotide 459 to nucleotide 539, and extending contiguously from a nucleotide sequence  
corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide  
539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from  
nucleotide 459 to nucleotide 539.

30 In other embodiments, the present invention provides a composition comprising a protein,  
wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment  
comprising eight contiguous amino acids of SEQ ID NO:16; and

- (c) the amino acid sequence encoded by the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196;  
the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 8 to amino acid 17 of SEQ ID NO:16.
- 10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944;
  - 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072;
  - (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO365\_2 deposited with the ATCC under accession number 98196;
  - 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;
  - (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO365\_2 deposited with the ATCC under accession number 98196;
  - 25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;
  - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:19;
  - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:19;
  - 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
  - (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
  - 35

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:18.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944; the nucleotide sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072; the nucleotide sequence of the full-length protein coding sequence of clone BO365\_2 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BO365\_2 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:19, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment comprising the amino acid sequence from amino acid 113 to amino acid 122 of SEQ ID NO:19.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:18.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:18, but excluding the poly(A) tail at the 3' end of SEQ ID NO:18; and

(ab) the nucleotide sequence of the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:18, but excluding the poly(A) tail at the 3' end of SEQ ID NO:18; and

(bb) the nucleotide sequence of the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:18, and extending contiguously  
15 from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:18 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:18, but excluding the poly(A) tail at the 3' end of SEQ ID NO:18. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944, and extending contiguously from a nucleotide sequence corresponding  
20 to the 5' end of said sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072, and extending contiguously from a nucleotide  
25 sequence corresponding to the 5' end of said sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:19;

(b) a fragment of the amino acid sequence of SEQ ID NO:19, the fragment comprising eight contiguous amino acids of SEQ ID NO:19; and

(c) the amino acid sequence encoded by the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:19. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:19, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment comprising the amino acid sequence from amino acid 113 to amino acid 122 of SEQ ID NO:19.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:20;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV51\_1 deposited with the ATCC under accession number 98196;
- 15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV51\_1 deposited with the ATCC under accession number 98196;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:21;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:21;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:20.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328; the nucleotide sequence of the full-length protein coding sequence of clone BV51\_1 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BV51\_1 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:21, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:21.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:20 and SEQ ID NO:22.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:20;  
(ab) SEQ ID NO:22, but excluding the poly(A) tail at the 3' end of SEQ ID NO:22; and  
(ac) the nucleotide sequence of the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;  
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and  
(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:20;  
(bb) SEQ ID NO:22, but excluding the poly(A) tail at the 3' end of SEQ ID NO:22; and  
(bc) the nucleotide sequence of the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;  
10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;  
(iii) amplifying human DNA sequences; and  
(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:20 and SEQ ID NO:22, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:20 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:22, but excluding the poly(A) tail at the 3' end of SEQ ID NO:22. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:20, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
20 SEQ ID NO:20 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:20. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:21;  
30 (b) a fragment of the amino acid sequence of SEQ ID NO:21, the fragment comprising eight contiguous amino acids of SEQ ID NO:21; and  
(c) the amino acid sequence encoded by the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein  
35 comprises the amino acid sequence of SEQ ID NO:21. In further preferred embodiments, the



present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:21, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment  
5 comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:21.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24  
10 from nucleotide 57 to nucleotide 396;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV140\_3 deposited with the ATCC under accession number 98196;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA  
15 insert of clone BV140\_3 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV140\_3 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert  
20 of clone BV140\_3 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment comprising eight  
25 contiguous amino acids of SEQ ID NO:25;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:24.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396; the nucleotide sequence of the full-length protein coding sequence of clone BV140\_3 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BV140\_3 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV140\_3 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25 from amino acid 29 to amino acid 57. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:25, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:25.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:24, SEQ ID NO:23, and SEQ ID NO:26.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:23;
    - 25 (ab) SEQ ID NO:24;
    - (ac) SEQ ID NO:26, but excluding the poly(A) tail at the 3' end of SEQ ID NO:26; and
    - (ad) the nucleotide sequence of the cDNA insert of clone BV140\_3 deposited with the ATCC under accession number 98196;
    - 30 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

-28-

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:23;  
(bb) SEQ ID NO:24;  
(bc) SEQ ID NO:26, but excluding the poly(A) tail at the 3' end of SEQ ID NO:26; and  
(bd) the nucleotide sequence of the cDNA insert of clone BV140\_3 deposited with the ATCC under accession number 98196;  
10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;  
(iii) amplifying human DNA sequences; and  
(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
15 sequence corresponding to the cDNA sequences of SEQ ID NO:23, SEQ ID NO:24, and SEQ ID NO:26, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:26, but excluding the poly(A) tail at the 3' end of SEQ ID NO:26. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the  
20 cDNA sequence of SEQ ID NO:24, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:24 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:24. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396, and extending contiguously from a nucleotide sequence  
25 corresponding to the 5' end of said sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 30 (a) the amino acid sequence of SEQ ID NO:25;  
(b) the amino acid sequence of SEQ ID NO:25 from amino acid 29 to amino acid 57;  
(c) a fragment of the amino acid sequence of SEQ ID NO:25, the fragment comprising eight contiguous amino acids of SEQ ID NO:25; and

(d) the amino acid sequence encoded by the cDNA insert of clone BV140\_3 deposited with the ATCC under accession number 98196; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:25 or the amino acid sequence of SEQ ID NO:25 from amino acid 29 to amino acid 57. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:25, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:25.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV141\_2 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV141\_2 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV141\_2 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV141\_2 deposited with the ATCC under accession number 98196;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328; the nucleotide sequence of SEQ ID NO:27 from  
10 nucleotide 1 to nucleotide 197; the nucleotide sequence of the full-length protein coding sequence of clone BV141\_2 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BV141\_2 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV141\_2 deposited with the  
15 ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight  
20 (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
25 NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

35 (ab) the nucleotide sequence of the cDNA insert of clone BV141\_2 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

5 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone BV141\_2 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence  
20 corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328, to a  
25 nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 1 to  
30 nucleotide 197, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 37;

(c) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

5 (d) the amino acid sequence encoded by the cDNA insert of clone BV141\_2 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28 or the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 37. In further preferred embodiments, the present  
10 invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:28.

15 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CC194\_4 deposited with the ATCC under accession number 98196;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CC194\_4 deposited with the ATCC under accession number 98196;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351; the nucleotide sequence of SEQ ID NO:29 from nucleotide  
15 328 to nucleotide 351; the nucleotide sequence of the full-length protein coding sequence of clone CC194\_4 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone CC194\_4 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CC194\_4 deposited with the ATCC under  
20 accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30 from amino acid 56 to amino acid 108. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more  
25 preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
30 NO:29 and SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:



(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:29;

5 (ab) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ac) the nucleotide sequence of the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29;

(bb) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

20 (bc) the nucleotide sequence of the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

25 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:29 and SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 28 to

30

35

nucleotide 351, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351. Also preferably the polynucleotide isolated according to the above process  
5 comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- (b) the amino acid sequence of SEQ ID NO:30 from amino acid 56 to amino acid 108;
- 15 (c) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein  
20 comprises the amino acid sequence of SEQ ID NO:30 or the amino acid sequence of SEQ ID NO:30 from amino acid 56 to amino acid 108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a  
25 fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32;
- 30 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DA136\_11 deposited with the ATCC under accession number 98196;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DA136\_11 deposited with the ATCC under accession number 98196;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:33;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:33;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:32.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198; the nucleotide sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058; the nucleotide sequence of the full-length protein coding sequence of clone DA136\_11 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone DA136\_11 deposited with the
- 30 ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:33 from amino acid 124 to amino acid 182. In further preferred
- 35 embodiments, the present invention provides a polynucleotide encoding a protein comprising a

fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:33, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:33.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:32.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 15 (aa) SEQ ID NO:32, but excluding the poly(A) tail at the 3' end of SEQ ID NO:32; and
    - (ab) the nucleotide sequence of the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (ba) SEQ ID NO:32, but excluding the poly(A) tail at the 3' end of SEQ ID NO:32; and
    - (bb) the nucleotide sequence of the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;
    - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
    - (iii) amplifying human DNA sequences; and
    - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:32, and extending contiguously

from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:32 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:32, but excluding the poly(A) tail at the 3' end of SEQ ID NO:32. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:33;
- (b) the amino acid sequence of SEQ ID NO:33 from amino acid 124 to amino acid 182;
- (c) a fragment of the amino acid sequence of SEQ ID NO:33, the fragment comprising eight contiguous amino acids of SEQ ID NO:33; and
- (d) the amino acid sequence encoded by the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:33 or the amino acid sequence of SEQ ID NO:33 from amino acid 124 to amino acid 182. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:33, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:33.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159;
- 5 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AR415\_4 deposited with the ATCC under accession number 98232;
- 10 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AR415\_4 deposited with the ATCC under accession number 98232;
- 15 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:35;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:35;
- 20 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:34.
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159; the nucleotide sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159; the nucleotide sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099; the nucleotide sequence of the full-length protein coding sequence of clone AR415\_4 deposited with the ATCC under accession number 98232; or the nucleotide

35

sequence of a mature protein coding sequence of clone AR415\_4 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:35 from amino acid 51 to amino acid 221. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:35, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:35.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:34.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:34, but excluding the poly(A) tail at the 3' end of SEQ ID NO:34; and

(ab) the nucleotide sequence of the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:34, but excluding the poly(A) tail at the 3' end of SEQ ID NO:34; and

- (bb) the nucleotide sequence of the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:34 to a nucleotide sequence

10 corresponding to the 3' end of SEQ ID NO:34, but excluding the poly(A) tail at the 3' end of SEQ ID NO:34. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159, to a

15 nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:34 from nucleotide 515 to

20 nucleotide 1159, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:34 from

25 nucleotide 539 to nucleotide 1099, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:35;
- 30 (b) the amino acid sequence of SEQ ID NO:35 from amino acid 51 to amino acid 221;
- (c) a fragment of the amino acid sequence of SEQ ID NO:35, the fragment comprising eight contiguous amino acids of SEQ ID NO:35; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AR415\_4
- 35 deposited with the ATCC under accession number 98232;



the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:35 or the amino acid sequence of SEQ ID NO:35 from amino acid 51 to amino acid 221. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:35, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:35.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:36;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AS63\_29 deposited with the ATCC under accession number 98232;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AS63\_29 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:37;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:37;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:36.

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376; the nucleotide sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376; the nucleotide sequence of the full-length protein coding sequence of clone AS63\_29 deposited with the ATCC under accession number 98232; or the nucleotide sequence  
10 of a mature protein coding sequence of clone AS63\_29 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:37 from  
15 amino acid 1 to amino acid 91. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:37, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having  
20 biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:37.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:36 and SEQ ID NO:38.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30

(aa) SEQ ID NO:36;

(ab) SEQ ID NO:38, but excluding the poly(A) tail at the 3' end of SEQ ID NO:38; and

(ac) the nucleotide sequence of the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- 5 (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (ba) SEQ ID NO:36;
- (bb) SEQ ID NO:38, but excluding the poly(A) tail at the 3' end of SEQ ID NO:38; and
- (bc) the nucleotide sequence of the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions
- 15 at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:36 and SEQ ID NO:38, and

20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:36 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:38, but excluding the poly(A) tail at the 3' end of SEQ ID NO:38. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:36, and extending contiguously from a nucleotide sequence corresponding to the 5' end of

25 SEQ ID NO:36 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:36. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376, to a nucleotide

30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide

376, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 5 (a) the amino acid sequence of SEQ ID NO:37;
- (b) the amino acid sequence of SEQ ID NO:37 from amino acid 1 to amino acid 91;
- (c) a fragment of the amino acid sequence of SEQ ID NO:37, the fragment comprising eight contiguous amino acids of SEQ ID NO:37; and
- 10 (d) the amino acid sequence encoded by the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:37 or the amino acid sequence of SEQ ID NO:37 from amino acid 1 to amino acid 91. In further preferred embodiments, the present  
15 invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:37, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:37.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039;
- 25 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AY304\_14 deposited with the ATCC under accession number 98561;
- 30 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AY304\_14 deposited with the ATCC under accession number 98561;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039; the nucleotide sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809; the nucleotide sequence of the full-length protein coding sequence of clone AY304\_14 deposited with the ATCC under accession number 98561; or the nucleotide sequence of a mature protein coding sequence of clone AY304\_14 deposited with the ATCC under accession number 98561. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40 from amino acid 106 to amino acid 204. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 302 to amino acid 311 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(ab) the nucleotide sequence of the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(bb) the nucleotide sequence of the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from

nucleotide 198 to nucleotide 2039. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
- 10 (b) the amino acid sequence of SEQ ID NO:40 from amino acid 106 to amino acid 204;
- (c) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AY304\_14
- 15 deposited with the ATCC under accession number 98561;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40 or the amino acid sequence of SEQ ID NO:40 from amino acid 106 to amino acid 204. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40

20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 302 to amino acid 311 of SEQ ID NO:40.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027;
- 30 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- 15 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:41.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027; the nucleotide sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027; the nucleotide sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431; the nucleotide sequence of the full-length protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence
- 30 of a mature protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42 from
- 35 amino acid 1 to amino acid 110. In further preferred embodiments, the present invention provides



a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having  
5 biological activity, the fragment comprising the amino acid sequence from amino acid 316 to amino acid 325 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

30 (bb) the nucleotide sequence of the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 207, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 207. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 207, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 207. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
  - (b) the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42 or the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a

fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 316 to amino acid 325 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO432\_4 deposited with the ATCC under accession number 98232;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO432\_4 deposited with the ATCC under accession number 98232;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:45;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:45;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:44.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631; the nucleotide sequence of the full-length protein coding sequence of clone BO432\_4 deposited with the ATCC under accession number 98232; or the  
35 nucleotide sequence of a mature protein coding sequence of clone BO432\_4 deposited with the

ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:45, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment comprising the amino acid sequence from amino acid 6 to amino acid 15 of SEQ ID NO:45.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:44, SEQ ID NO:43, and SEQ ID NO:46.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:43;
      - (ab) SEQ ID NO:44;
      - (ac) SEQ ID NO:46, but excluding the poly(A) tail at the 3' end of SEQ ID NO:46; and
      - (ad) the nucleotide sequence of the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:43;
      - (bb) SEQ ID NO:44;
      - (bc) SEQ ID NO:46, but excluding the poly(A) tail at the 3' end of SEQ ID NO:46; and

- (bd) the nucleotide sequence of the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:43, SEQ ID NO:44, and SEQ ID NO:46, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:46, but excluding the poly(A) tail at the 3' end of SEQ ID NO:46. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:44, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:44 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:44. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:45;
- (b) a fragment of the amino acid sequence of SEQ ID NO:45, the fragment comprising eight contiguous amino acids of SEQ ID NO:45; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:45. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:45, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment comprising the amino acid sequence from amino acid 6 to amino acid 15 of SEQ ID NO:45.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47  
5 from nucleotide 45 to nucleotide 428;
  - (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO538\_2 deposited with the ATCC under accession number 98232;
  - (d) a polynucleotide encoding the full-length protein encoded by the cDNA  
10 insert of clone BO538\_2 deposited with the ATCC under accession number 98232;
  - (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO538\_2 deposited with the ATCC under accession number 98232;
  - (f) a polynucleotide encoding a mature protein encoded by the cDNA insert  
15 of clone BO538\_2 deposited with the ATCC under accession number 98232;
  - (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
  - (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight  
20 contiguous amino acids of SEQ ID NO:48;
  - (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
  - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
  - (k) a polynucleotide that hybridizes under stringent conditions to any one of  
25 the polynucleotides specified in (a)-(h); and
  - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:47.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428; the nucleotide sequence of the full-length protein coding sequence of clone BO538\_2 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone BO538\_2 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide  
35 encodes the full-length or a mature protein encoded by the cDNA insert of clone BO538\_2

deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48 from amino acid 52 to amino acid 128. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:48.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47 and SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:47;  
(ab) SEQ ID NO:49, but excluding the poly(A) tail at the 3'  
20 end of SEQ ID NO:49; and  
(ac) the nucleotide sequence of the cDNA insert of clone BO538\_2 deposited with the ATCC under accession number 98232;  
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and  
25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:  
(i) preparing one or more polynucleotide primers that hybridize in  
30 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:47;  
(bb) SEQ ID NO:49, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:49; and  
(bc) the nucleotide sequence of the cDNA insert of clone  
35 BO538\_2 deposited with the ATCC under accession number 98232;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:47 and SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the
- 10 above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 45 to
- 15 nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428.

- In other embodiments, the present invention provides a composition comprising a protein,
- 20 wherein said protein comprises an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:48;
  - (b) the amino acid sequence of SEQ ID NO:48 from amino acid 52 to amino acid 128;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment
  - 25 comprising eight contiguous amino acids of SEQ ID NO:48; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BO538\_2 deposited with the ATCC under accession number 98232;

- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48 or the amino acid sequence of SEQ ID
- 30 NO:48 from amino acid 52 to amino acid 128. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment
- 35 comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:48.



In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50  
5 from nucleotide 144 to nucleotide 566;
  - (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BR595\_4 deposited with the ATCC under accession number 98232;
  - (d) a polynucleotide encoding the full-length protein encoded by the cDNA  
10 insert of clone BR595\_4 deposited with the ATCC under accession number 98232;
  - (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BR595\_4 deposited with the ATCC under accession number 98232;
  - (f) a polynucleotide encoding a mature protein encoded by the cDNA insert  
15 of clone BR595\_4 deposited with the ATCC under accession number 98232;
  - (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:51;
  - (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment comprising eight  
20 contiguous amino acids of SEQ ID NO:51;
  - (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
  - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
  - (k) a polynucleotide that hybridizes under stringent conditions to any one of  
25 the polynucleotides specified in (a)-(h); and
  - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:50.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566; the nucleotide sequence of the full-length protein coding sequence of clone BR595\_4 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone BR595\_4 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide  
35 encodes the full-length or a mature protein encoded by the cDNA insert of clone BR595\_4

deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:51 from amino acid 39 to amino acid 141. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:51, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:51.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:50 and SEQ ID NO:52.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:50;
    - (ab) SEQ ID NO:52, but excluding the poly(A) tail at the 3'  
20 end of SEQ ID NO:52; and
    - (ac) the nucleotide sequence of the cDNA insert of clone BR595\_4 deposited with the ATCC under accession number 98232;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in  
30 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:50;
    - (bb) SEQ ID NO:52, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:52; and
    - (bc) the nucleotide sequence of the cDNA insert of clone  
35 BR595\_4 deposited with the ATCC under accession number 98232;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:50 and SEQ ID NO:52, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:50 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:52, but excluding the poly(A) tail at the 3' end of SEQ ID NO:52. Also preferably the polynucleotide isolated according to the
- 10 above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:50, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:50 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:50. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:50 from nucleotide 144 to
- 15 nucleotide 566, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566.

- In other embodiments, the present invention provides a composition comprising a protein,
- 20 wherein said protein comprises an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:51;
  - (b) the amino acid sequence of SEQ ID NO:51 from amino acid 39 to amino acid 141;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:51, the fragment
  - 25 comprising eight contiguous amino acids of SEQ ID NO:51; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BR595\_4 deposited with the ATCC under accession number 98232;

- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:51 or the amino acid sequence of SEQ ID
- 30 NO:51 from amino acid 39 to amino acid 141. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:51, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment
- 35 comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:51.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53  
5 from nucleotide 232 to nucleotide 1041;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53  
from nucleotide 460 to nucleotide 1041;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53  
from nucleotide 590 to nucleotide 1163;
- 10 (e) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone CI490\_2 deposited with the ATCC under accession  
number 98232;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone CI490\_2 deposited with the ATCC under accession number 98232;
- 15 (g) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone CI490\_2 deposited with the ATCC under accession number  
98232;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone CI490\_2 deposited with the ATCC under accession number 98232;
- 20 (i) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:54;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight  
contiguous amino acids of SEQ ID NO:54;
- 25 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)  
above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i)  
or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the  
length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53  
35 from nucleotide 232 to nucleotide 1041; the nucleotide sequence of SEQ ID NO:53 from

nucleotide 460 to nucleotide 1041; the nucleotide sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163; the nucleotide sequence of the full-length protein coding sequence of clone CI490\_2 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CI490\_2 deposited with the ATCC under  
5 accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CI490\_2 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54 from amino acid 133 to amino acid 270. In further preferred embodiments, the present  
10 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino  
15 acid 130 to amino acid 139 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3'  
25 end of SEQ ID NO:53; and
    - (ab) the nucleotide sequence of the cDNA insert of clone CI490\_2 deposited with the ATCC under accession number 98232;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
35 consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone CI490\_2 deposited with the ATCC under accession number 98232;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
10 sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide  
15 232 to nucleotide 1041, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 232 to nucleotide 1041, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 232 to nucleotide 1041. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
20 NO:53 from nucleotide 460 to nucleotide 1041, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 460 to nucleotide 1041, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 460 to nucleotide 1041. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA  
25 sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163.

In other embodiments, the present invention provides a composition comprising a protein,  
30 wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) the amino acid sequence of SEQ ID NO:54 from amino acid 133 to amino acid 270;

(c) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment  
35 comprising eight contiguous amino acids of SEQ ID NO:54; and

(d) the amino acid sequence encoded by the cDNA insert of clone CI490\_2 deposited with the ATCC under accession number 98232; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54 or the amino acid sequence of SEQ ID NO:54 from amino acid 133 to amino acid 270. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 130 to amino acid 139 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CI522\_1 deposited with the ATCC under accession number 98232;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CI522\_1 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624; the nucleotide sequence of SEQ ID NO:55 from nucleotide  
10 325 to nucleotide 624; the nucleotide sequence of the full-length protein coding sequence of clone CI522\_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CI522\_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CI522\_1 deposited with the ATCC under  
15 accession number 98232. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide  
20 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55 and SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:55;  
(ab) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and  
(ac) the nucleotide sequence of the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;



(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

5

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:55;

10

(bb) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(bc) the nucleotide sequence of the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;

15

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:55 and SEQ ID NO:57, and  
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
25 SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624, to a nucleotide  
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide

624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 5 (a) the amino acid sequence of SEQ ID NO:56;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;
- 10 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising
- 15 a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:58;
- 20 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CN238\_1 deposited with the ATCC under accession number 98232;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CN238\_1 deposited with the ATCC under accession number 98232;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence
- 35 of SEQ ID NO:59;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:59;
- 5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:58.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710; the nucleotide sequence of SEQ ID NO:58 from  
15 nucleotide 868 to nucleotide 1887; the nucleotide sequence of the full-length protein coding sequence of clone CN238\_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CN238\_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CN238\_1  
20 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:59 from amino acid 1 to amino acid 109. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment  
25 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:59, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:59.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
30 NO:58.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:58, but excluding the poly(A) tail at the 3' end of SEQ ID NO:58; and

(ab) the nucleotide sequence of the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:58, but excluding the poly(A) tail at the 3' end of SEQ ID NO:58; and

(bb) the nucleotide sequence of the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:58, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:58 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:58, but excluding the poly(A) tail at the 3' end of SEQ ID NO:58. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887, and extending contiguously from a nucleotide

sequence corresponding to the 5' end of said sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887.

In other embodiments, the present invention provides a composition comprising a protein,  
5 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:59;
- (b) the amino acid sequence of SEQ ID NO:59 from amino acid 1 to amino acid 109;
- (c) a fragment of the amino acid sequence of SEQ ID NO:59, the fragment  
10 comprising eight contiguous amino acids of SEQ ID NO:59; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:59 or the amino acid sequence of SEQ ID  
15 NO:59 from amino acid 1 to amino acid 109. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:59, or a protein comprising a  
20 fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:59.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:60;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:60  
25 from nucleotide 87 to nucleotide 1871;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO390\_1 deposited with the ATCC under accession  
30 number 98232;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO390\_1 deposited with the ATCC under accession number  
35 98232;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:61;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:61;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of
- 15 the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:60.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871; the nucleotide sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882; the nucleotide sequence of the full-length protein coding
- 20 sequence of clone CO390\_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CO390\_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232. In yet other preferred embodiments,
- 25 the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:61 from amino acid 182 to amino acid 248. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino
- 30 acids of SEQ ID NO:61, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment comprising the amino acid sequence from amino acid 292 to amino acid 301 of SEQ ID NO:61.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:60.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

5 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:60, but excluding the poly(A) tail at the 3' end of SEQ ID NO:60; and

10 (ab) the nucleotide sequence of the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

15 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:60, but excluding the poly(A) tail at the 3' end of SEQ ID NO:60; and

(bb) the nucleotide sequence of the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:60, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:60 to a nucleotide sequence  
30 corresponding to the 3' end of SEQ ID NO:60, but excluding the poly(A) tail at the 3' end of SEQ ID NO:60. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871, to a  
35 nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:60 from

nucleotide 87 to nucleotide 1871. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:61;
- 10 (b) the amino acid sequence of SEQ ID NO:61 from amino acid 182 to amino acid 248;
- (c) a fragment of the amino acid sequence of SEQ ID NO:61, the fragment comprising eight contiguous amino acids of SEQ ID NO:61; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CO390\_1
- 15 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:61 or the amino acid sequence of SEQ ID NO:61 from amino acid 182 to amino acid 248. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61

20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:61, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment comprising the amino acid sequence from amino acid 292 to amino acid 301 of SEQ ID NO:61.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:62;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430;
- 30 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AJ20\_2 deposited with the ATCC under accession number 98261;



- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:63;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:63;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:62.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430; the nucleotide sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430; the nucleotide sequence of the full-length protein coding sequence of clone AJ20\_2 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AJ20\_2 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:63, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:63.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:62 and SEQ ID NO:64.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:62;
- (ab) SEQ ID NO:64, but excluding the poly(A) tail at the 3' end of SEQ ID NO:64; and
- (ac) the nucleotide sequence of the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- 15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in
- 20 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:62;
- (bb) SEQ ID NO:64, but excluding the poly(A) tail at the 3' end of SEQ ID NO:64; and
- 25 (bc) the nucleotide sequence of the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 30 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:62 and SEQ ID NO:64, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:62 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:64, but excluding the poly(A) tail at the 3' end of SEQ ID NO:64. Also preferably the polynucleotide isolated according to the

35

above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:62, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:62 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:62. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:63;
- (b) a fragment of the amino acid sequence of SEQ ID NO:63, the fragment comprising eight contiguous amino acids of SEQ ID NO:63; and
- (c) the amino acid sequence encoded by the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:63. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:63, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:63.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:66;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AR440\_1 deposited with the ATCC under accession number 98261;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AR440\_1 deposited with the ATCC under accession number 98261;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:67;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment comprising eight  
15 contiguous amino acids of SEQ ID NO:67;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:66.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780; the nucleotide sequence of the full-length protein coding sequence of clone AR440\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AR440\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide  
30 encodes the full-length or a mature protein encoded by the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:67 from amino acid 1 to amino acid 160. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
35 fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:67, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:67.

5           Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:66 and SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 10           (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:65;
    - (ab) SEQ ID NO:66, but excluding the poly(A) tail at the 3'
    - 15           end of SEQ ID NO:66; and
    - (ac) the nucleotide sequence of the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 20           (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
  - 25           consisting of:
    - (ba) SEQ ID NO:65;
    - (bb) SEQ ID NO:66, but excluding the poly(A) tail at the 3'
    - end of SEQ ID NO:66; and
    - (bc) the nucleotide sequence of the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261;
    - 30           (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
    - (iii) amplifying human DNA sequences; and
    - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:65 and SEQ ID NO:66, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:66, but excluding the poly(A) tail at the 3' end of SEQ ID NO:66. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:66, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:66 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:66, but excluding the poly(A) tail at the 3' end of SEQ ID NO:66. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:67;
- (b) the amino acid sequence of SEQ ID NO:67 from amino acid 1 to amino acid 160;
- (c) a fragment of the amino acid sequence of SEQ ID NO:67, the fragment comprising eight contiguous amino acids of SEQ ID NO:67; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:67 or the amino acid sequence of SEQ ID NO:67 from amino acid 1 to amino acid 160. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:67, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:67.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:68;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AS164\_1 deposited with the ATCC under accession number 98261;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AS164\_1 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:69;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:69;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:68.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050; the nucleotide sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567; the nucleotide sequence of the full-length protein coding sequence of clone AS164\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AS164\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide

30 encodes the full-length or a mature protein encoded by the cDNA insert of clone AS164\_1

35

deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:69 from amino acid 87 to amino acid 164. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:69, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment comprising the amino acid sequence from amino acid 157 to amino acid 166 of SEQ ID NO:69.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:68.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:68, but excluding the poly(A) tail at the 3' end of SEQ ID NO:68; and

20 (ab) the nucleotide sequence of the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

25 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:68, but excluding the poly(A) tail at the 3' end of SEQ ID NO:68; and

(bb) the nucleotide sequence of the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;

35 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;



- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:68, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:68 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:68, but excluding the poly(A) tail at the 3' end of SEQ ID NO:68. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:69;
- (b) the amino acid sequence of SEQ ID NO:69 from amino acid 87 to amino acid 164;
- (c) a fragment of the amino acid sequence of SEQ ID NO:69, the fragment comprising eight contiguous amino acids of SEQ ID NO:69; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:69 or the amino acid sequence of SEQ ID NO:69 from amino acid 87 to amino acid 164. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:69, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment comprising the amino acid sequence from amino acid 157 to amino acid 166 of SEQ ID NO:69.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70  
5 from nucleotide 242 to nucleotide 1060;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70  
from nucleotide 596 to nucleotide 1060;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70  
from nucleotide 10 to nucleotide 373;
- 10 (e) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone AX8\_1 deposited with the ATCC under accession  
number 98261;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone AX8\_1 deposited with the ATCC under accession number 98261;
- 15 (g) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone AX8\_1 deposited with the ATCC under accession number  
98261;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone AX8\_1 deposited with the ATCC under accession number 98261;
- 20 (i) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:71;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:71 having biological activity, the fragment comprising eight  
contiguous amino acids of SEQ ID NO:71;
- 25 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)  
above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i)  
or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the  
length of SEQ ID NO:70.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:70  
35 from nucleotide 242 to nucleotide 1060; the nucleotide sequence of SEQ ID NO:70 from

nucleotide 596 to nucleotide 1060; the nucleotide sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373; the nucleotide sequence of the full-length protein coding sequence of clone AX8\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AX8\_1 deposited with the ATCC under accession  
5 number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AX8\_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:71 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides  
10 a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:71, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to  
15 amino acid 140 of SEQ ID NO:71.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:70.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:70, but excluding the poly(A) tail at the 3'  
25 end of SEQ ID NO:70; and
- (ab) the nucleotide sequence of the cDNA insert of clone AX8\_1 deposited with the ATCC under accession number 98261;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
35 consisting of:

- (ba) SEQ ID NO:70, but excluding the poly(A) tail at the 3' end of SEQ ID NO:70; and
- (bb) the nucleotide sequence of the cDNA insert of clone AX8\_1 deposited with the ATCC under accession number 98261;
- 5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
10 sequence corresponding to the cDNA sequence of SEQ ID NO:70, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:70 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:70, but excluding the poly(A) tail at the 3' end of SEQ ID NO:70. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:70 from nucleotide  
15 242 to nucleotide 1060, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:70 from nucleotide 242 to nucleotide 1060, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:70 from nucleotide 242 to nucleotide 1060. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
20 NO:70 from nucleotide 596 to nucleotide 1060, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:70 from nucleotide 596 to nucleotide 1060, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:70 from nucleotide 596 to nucleotide 1060. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA  
25 sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373.

In other embodiments, the present invention provides a composition comprising a protein,  
30 wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:71;

(b) the amino acid sequence of SEQ ID NO:71 from amino acid 1 to amino acid 44;

(c) a fragment of the amino acid sequence of SEQ ID NO:71, the fragment  
35 comprising eight contiguous amino acids of SEQ ID NO:71; and

(d) the amino acid sequence encoded by the cDNA insert of clone AX8\_1 deposited with the ATCC under accession number 98261; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:71 or the amino acid sequence of SEQ ID NO:71 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:71, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:71.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:72;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD176\_3 deposited with the ATCC under accession number 98261;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD176\_3 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:73;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:73;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:72.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928; the nucleotide sequence of SEQ ID NO:72 from nucleotide  
10 815 to nucleotide 928; the nucleotide sequence of the full-length protein coding sequence of clone BD176\_3 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BD176\_3 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD176\_3 deposited with the ATCC under  
15 accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:73, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having  
20 biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:73.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:72 and SEQ ID NO:74.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30

(aa) SEQ ID NO:72;

(ab) SEQ ID NO:74, but excluding the poly(A) tail at the 3' end of SEQ ID NO:74; and

(ac) the nucleotide sequence of the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

5 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:72;

10 (bb) SEQ ID NO:74, but excluding the poly(A) tail at the 3' end of SEQ ID NO:74; and

(bc) the nucleotide sequence of the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:72 and SEQ ID NO:74, and  
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:72 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:74, but excluding the poly(A) tail at the 3' end of SEQ ID NO:74. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:72, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
25 SEQ ID NO:72 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:72. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928, to a nucleotide  
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide

928, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 5           (a)     the amino acid sequence of SEQ ID NO:73;
- (b)     a fragment of the amino acid sequence of SEQ ID NO:73, the fragment comprising eight contiguous amino acids of SEQ ID NO:73; and
- (c)     the amino acid sequence encoded by the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;
- 10   the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:73. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:73, or a protein comprising
- 15   a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:73.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- 20          (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD339\_1 deposited with the ATCC under accession
- 25          number 98261;
- (e)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD339\_1 deposited with the ATCC under accession number
- 30          98261;
- (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;
- (h)     a polynucleotide encoding a protein comprising the amino acid sequence
- 35          of SEQ ID NO:76;



(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440; the nucleotide sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313; the nucleotide sequence of the full-length protein coding sequence of clone BD339\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BD339\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76 from amino acid 1 to amino acid 46. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(ab) the nucleotide sequence of the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313, and extending contiguously from a nucleotide

sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313.

In other embodiments, the present invention provides a composition comprising a protein,  
5 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
- (b) the amino acid sequence of SEQ ID NO:76 from amino acid 1 to amino acid 46;
- (c) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment  
10 comprising eight contiguous amino acids of SEQ ID NO:76; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76 or the amino acid sequence of SEQ ID  
15 NO:76 from amino acid 1 to amino acid 46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment  
20 comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77  
25 from nucleotide 509 to nucleotide 619;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD427\_1 deposited with the ATCC under accession  
30 number 98261;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD427\_1 deposited with the ATCC under accession number  
35 98261;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of
- 15 the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619; the nucleotide sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580; the nucleotide sequence of the full-length protein coding sequence of clone BD427\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BD427\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention

20 provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 24. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a

25 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 13 to amino acid 22 of SEQ ID NO:78.

30

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

5 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

10 (ab) the nucleotide sequence of the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

15 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(bb) the nucleotide sequence of the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence  
30 corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619, to a  
35 nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from

nucleotide 509 to nucleotide 619. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- 10 (b) the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 24;
- (c) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BD427\_1
- 15 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78 or the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 13 to amino acid 22 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BL229\_22 deposited with the ATCC under accession number 98261;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BL229\_22 deposited with the ATCC under accession number 98261;
- 5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight  
10 contiguous amino acids of SEQ ID NO:80;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 15 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:79.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360; the nucleotide sequence of the full-length protein coding sequence of clone BL229\_22 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BL229\_22 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide  
25 encodes the full-length or a mature protein encoded by the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ  
30 ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 5 to amino acid 14 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79 and SEQ ID NO:81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:79;

(ab) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(ac) the nucleotide sequence of the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79;

(bb) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bc) the nucleotide sequence of the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:79 and SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of



SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:80;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising
- 20 a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 5 to amino acid 14 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:82;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV123\_16 deposited with the ATCC under accession
- 30 number 98261;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV123\_16 deposited with the ATCC under accession number 98261;
- 5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:83;
- 10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:83;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:82.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771; the nucleotide sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684; the nucleotide sequence of the full-length protein coding sequence of clone BV123\_16 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BV123\_16 deposited with the ATCC under
- 25 accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:83 from amino acid 1 to amino acid 27. In further preferred embodiments, the present
- 30 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:83, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment comprising the amino acid sequence from amino
- 35 acid 23 to amino acid 32 of SEQ ID NO:83.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:82.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82; and
- (ab) the nucleotide sequence of the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 20 consisting of:
- (ba) SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82; and
- (bb) the nucleotide sequence of the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;
- 25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide

30 sequence corresponding to the cDNA sequence of SEQ ID NO:82, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:82 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:82 from nucleotide

35 604 to nucleotide 771, and extending contiguously from a nucleotide sequence corresponding to

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:82.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82; and
- (ab) the nucleotide sequence of the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 20 (ba) SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82; and
- (bb) the nucleotide sequence of the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;
- 25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:82, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:82 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:82 from nucleotide 30 604 to nucleotide 771, and extending contiguously from a nucleotide sequence corresponding to

35

the 5' end of said sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
5 NO:82 from nucleotide 1 to nucleotide 684, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684.

In other embodiments, the present invention provides a composition comprising a protein,  
10 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:83;
- (b) the amino acid sequence of SEQ ID NO:83 from amino acid 1 to amino acid 27;
- (c) a fragment of the amino acid sequence of SEQ ID NO:83, the fragment  
15 comprising eight contiguous amino acids of SEQ ID NO:83; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:83 or the amino acid sequence of SEQ ID  
20 NO:83 from amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:83, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment  
25 comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:83.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84  
30 from nucleotide 43 to nucleotide 297;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CH377\_1 deposited with the ATCC under accession number 98261;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CH377\_1 deposited with the ATCC under accession number 98261;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:85;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment comprising eight  
15 contiguous amino acids of SEQ ID NO:85;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:84.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297; the nucleotide sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297; the nucleotide sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379; the nucleotide sequence of the full-length protein coding sequence of clone CH377\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature  
30 protein coding sequence of clone CH377\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID  
35 NO:85 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:85, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:85.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:84.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:84, but excluding the poly(A) tail at the 3' end of SEQ ID NO:84; and
    - 15 (ab) the nucleotide sequence of the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
  - 20 and
  - (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - 25 (ba) SEQ ID NO:84, but excluding the poly(A) tail at the 3' end of SEQ ID NO:84; and
      - (bb) the nucleotide sequence of the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
      - (ii) hybridizing said primer(s) to human genomic DNA in conditions
      - 30 at least as stringent as 4X SSC at 50 degrees C;
      - (iii) amplifying human DNA sequences; and
      - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:84 to a nucleotide sequence

35

corresponding to the 3' end of SEQ ID NO:84, but excluding the poly(A) tail at the 3' end of SEQ ID NO:84. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:85;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:85, the fragment comprising eight contiguous amino acids of SEQ ID NO:85; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:85. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:85, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:85.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;



- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD441\_1 deposited with the ATCC under accession number 98264;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD441\_1 deposited with the ATCC under accession number 98264;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- 15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 20 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of 25 the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563; the nucleotide sequence of the full-length protein coding sequence of clone BD441\_1 deposited with the ATCC under accession number 98264; or the 30 nucleotide sequence of a mature protein coding sequence of clone BD441\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the 35 amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:88.

- 5           Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87, SEQ ID NO:86, and SEQ ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10           (a)    a process comprising the steps of:  
              (i)    preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 15                       (aa)   SEQ ID NO:86;  
                      (ab)   SEQ ID NO:87;  
                      (ac)   SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and  
                      (ad)   the nucleotide sequence of the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;  
20               (ii)   hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and  
              (iii)   isolating the DNA polynucleotides detected with the probe(s);

and

- (b)    a process comprising the steps of:  
              (i)    preparing one or more polynucleotide primers that hybridize in  
25               6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba)   SEQ ID NO:86;  
                      (bb)   SEQ ID NO:87;  
                      (bc)   SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and  
30                       (bd)   the nucleotide sequence of the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;  
                      (ii)   hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;  
35               (iii)   amplifying human DNA sequences; and

## (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:86, SEQ ID NO:87, and SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:86 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;
- (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:90;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD441\_2 deposited with the ATCC under accession number 98264;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD441\_2 deposited with the ATCC under accession number 98264;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD441\_2 deposited with the ATCC under accession number 98264;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD441\_2 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:91;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment comprising eight  
15 contiguous amino acids of SEQ ID NO:91;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:90.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756; the nucleotide sequence of the full-length protein coding sequence of clone BD441\_2 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BD441\_2 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide  
30 encodes the full-length or a mature protein encoded by the cDNA insert of clone BD441\_2 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ  
35 ID NO:91, or a polynucleotide encoding a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:91 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:91.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:90 and SEQ ID NO:92.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X  
10 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:90;

(ab) SEQ ID NO:92, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:92; and

(ac) the nucleotide sequence of the cDNA insert of clone  
15 BD441\_2 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in  
6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
consisting of:

(ba) SEQ ID NO:90;

25 (bb) SEQ ID NO:92, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:92; and

(bc) the nucleotide sequence of the cDNA insert of clone  
BD441\_2 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions  
30 at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
sequence corresponding to the cDNA sequences of SEQ ID NO:90 and SEQ ID NO:92, and  
35 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:90

to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:92, but excluding the poly(A) tail at the 3' end of SEQ ID NO:92. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:90, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
5 SEQ ID NO:90 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:90. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:91;
- 15 (b) a fragment of the amino acid sequence of SEQ ID NO:91, the fragment comprising eight contiguous amino acids of SEQ ID NO:91; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BD441\_2 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein  
20 comprises the amino acid sequence of SEQ ID NO:91. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:91, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment  
25 comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:91.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93  
30 from nucleotide 426 to nucleotide 581;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG102\_3 deposited with the ATCC under accession number 98264;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG102\_3 deposited with the ATCC under accession number 98264;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- 15 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:93.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581; the nucleotide sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581; the nucleotide sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503; the nucleotide sequence of the full-length protein coding sequence of clone BG102\_3 deposited with the ATCC under accession number 98264; or the nucleotide sequence
- 30 of a mature protein coding sequence of clone BG102\_3 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94 from
- 35 amino acid 1 to amino acid 26. In further preferred embodiments, the present invention provides

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having  
5 biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(ab) the nucleotide sequence of the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

30 (bb) the nucleotide sequence of the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).



Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
  - (b) the amino acid sequence of SEQ ID NO:94 from amino acid 1 to amino acid 26;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94 or the amino acid sequence of SEQ ID NO:94 from amino acid 1 to amino acid 26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a

fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95  
                  from nucleotide 112 to nucleotide 978;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95  
                  from nucleotide 436 to nucleotide 1048;
- 10                  (d)     a polynucleotide comprising the nucleotide sequence of the full-length  
                  protein coding sequence of clone BK158\_1 deposited with the ATCC under accession  
                  number 98264;
- (e)     a polynucleotide encoding the full-length protein encoded by the cDNA  
                  insert of clone BK158\_1 deposited with the ATCC under accession number 98264;
- 15                  (f)     a polynucleotide comprising the nucleotide sequence of a mature protein  
                  coding sequence of clone BK158\_1 deposited with the ATCC under accession number  
                  98264;
- (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert  
                  of clone BK158\_1 deposited with the ATCC under accession number 98264;
- 20                  (h)     a polynucleotide encoding a protein comprising the amino acid sequence  
                  of SEQ ID NO:96;
- (i)     a polynucleotide encoding a protein comprising a fragment of the amino  
                  acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight  
                  contiguous amino acids of SEQ ID NO:96;
- 25                  (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g)  
                  above;
- (k)     a polynucleotide which encodes a species homologue of the protein of (h)  
                  or (i) above ;
- (l)     a polynucleotide that hybridizes under stringent conditions to any one of  
30                  the polynucleotides specified in (a)-(i); and
- (m)     a polynucleotide that hybridizes under stringent conditions to any one of  
                  the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the  
                  length of SEQ ID NO:95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95  
35   from nucleotide 112 to nucleotide 978; the nucleotide sequence of SEQ ID NO:95 from

nucleotide 436 to nucleotide 1048; the nucleotide sequence of the full-length protein coding sequence of clone BK158\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BK158\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide  
5 encodes the full-length or a mature protein encoded by the cDNA insert of clone BK158\_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ  
10 ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:96.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X  
20 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:95; and

(ab) the nucleotide sequence of the cDNA insert of clone  
BK158\_1 deposited with the ATCC under accession number 98264;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:95; and

- (bb) the nucleotide sequence of the cDNA insert of clone BK158\_1 deposited with the ATCC under accession number 98264;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence

10 corresponding to the 3' end of SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978, to a

15 nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 436 to nucleotide 1048, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 436 to

20 nucleotide 1048, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 436 to nucleotide 1048.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:96;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BK158\_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein

30 comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment

35 comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97  
5 from nucleotide 16 to nucleotide 492;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BP163\_1 deposited with the ATCC under accession number 98264;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA  
10 insert of clone BP163\_1 deposited with the ATCC under accession number 98264;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BP163\_1 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert  
15 of clone BP163\_1 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight  
20 contiguous amino acids of SEQ ID NO:98;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of  
25 the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:97.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492; the nucleotide sequence of the full-length protein coding sequence of clone BP163\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BP163\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide  
35 encodes the full-length or a mature protein encoded by the cDNA insert of clone BP163\_1

deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:98.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97 and SEQ ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:97;

(ab) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(ac) the nucleotide sequence of the cDNA insert of clone BP163\_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:97;

(bb) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(bc) the nucleotide sequence of the cDNA insert of clone BP163\_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:97 and SEQ ID NO:99, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
10 SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492, to a nucleotide  
15 sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
- 20 (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BP163\_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein  
25 comprises the amino acid sequence of SEQ ID NO:98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment  
30 comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101  
35 from nucleotide 72 to nucleotide 569;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BZ16\_3 deposited with the ATCC under accession number 98264;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BZ16\_3 deposited with the ATCC under accession number 98264;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:101.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569; the nucleotide sequence of the full-length protein coding sequence of clone BZ16\_3 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BZ16\_3 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide  
30 encodes the full-length or a mature protein encoded by the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102 from amino acid 1 to amino acid 124. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
35 fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment



preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:102.

- 5           Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101 and SEQ ID NO:100.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a)     a process comprising the steps of:
- 10           (i)     preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa)   SEQ ID NO:100;
- (ab)   SEQ ID NO:101, but excluding the poly(A) tail at the 3'
- 15           end of SEQ ID NO:101; and
- (ac)   the nucleotide sequence of the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264;
- (ii)   hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 20           (iii)   isolating the DNA polynucleotides detected with the probe(s);
- and
- (b)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 25           consisting of:
- (ba)   SEQ ID NO:100;
- (bb)   SEQ ID NO:101, but excluding the poly(A) tail at the 3'
- end of SEQ ID NO:101; and
- (bc)   the nucleotide sequence of the cDNA insert of clone
- 30           BZ16\_3 deposited with the ATCC under accession number 98264;
- (ii)   hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii)   amplifying human DNA sequences; and
- (iv)   isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:100 and SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:100 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
  - (b) the amino acid sequence of SEQ ID NO:102 from amino acid 1 to amino acid 124;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102 or the amino acid sequence of SEQ ID NO:102 from amino acid 1 to amino acid 124. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662; \*
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662; the nucleotide sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662; the nucleotide sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584; the nucleotide sequence of the full-length protein coding sequence of clone

CC182\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone CC182\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CC182\_1 deposited with the ATCC under  
5 accession number 98264. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104 from amino acid 1 to amino acid 60. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably  
10 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
15 NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X  
20 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
    - (ab) the nucleotide sequence of the cDNA insert of clone  
25 CC182\_1 deposited with the ATCC under accession number 98264;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- 30 (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3'  
35 end of SEQ ID NO:103; and

- (bb) the nucleotide sequence of the cDNA insert of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide  
10 sequence corresponding to the 3' end of SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide  
15 662, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 519  
20 to nucleotide 662, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from  
25 nucleotide 1 to nucleotide 584, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- 30 (b) the amino acid sequence of SEQ ID NO:104 from amino acid 1 to amino acid 60;
- (c) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CC182\_1  
35 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104 or the amino acid sequence of SEQ ID NO:104 from amino acid 1 to amino acid 60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CG109\_1 deposited with the ATCC under accession number 98264;
- 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CG109\_1 deposited with the ATCC under accession number 98264;
- 25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 35

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409; the nucleotide sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414; the nucleotide sequence of the full-length protein coding sequence of clone CG109\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone CG109\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 11 to amino acid 20 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(ab) the nucleotide sequence of the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously  
15 from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409, and extending contiguously from a nucleotide sequence  
20 corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414, and extending contiguously from a nucleotide  
25 sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:106;

(b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

(c) the amino acid sequence encoded by the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;



the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably  
5 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 11 to amino acid 20 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated  
10 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:108;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length  
15 protein coding sequence of clone CJ397\_1 deposited with the ATCC under accession number 98264;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ397\_1 deposited with the ATCC under accession number 98264;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein  
20 coding sequence of clone CJ397\_1 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CJ397\_1 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence  
25 of SEQ ID NO:109;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:109;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f)  
30 above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:108.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:108  
5 from nucleotide 471 to nucleotide 611; the nucleotide sequence of the full-length protein coding sequence of clone CJ397\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone CJ397\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CJ397\_1  
10 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:109, or a polynucleotide encoding a protein comprising a fragment of the amino acid  
15 sequence of SEQ ID NO:109 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:109.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:108, SEQ ID NO:107, and SEQ ID NO:110.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X  
SSC at 65 degrees C to a nucleotide sequence selected from the group consisting  
of:

25 (aa) SEQ ID NO:107;  
(ab) SEQ ID NO:108;  
(ac) SEQ ID NO:110, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:110; and  
(ad) the nucleotide sequence of the cDNA insert of clone  
30 CJ397\_1 deposited with the ATCC under accession number 98264;  
(ii) hybridizing said probe(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C; and  
(iii) isolating the DNA polynucleotides detected with the probe(s);

and

35 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:107;  
(bb) SEQ ID NO:108;  
(bc) SEQ ID NO:110, but excluding the poly(A) tail at the 3' end of SEQ ID NO:110; and  
(bd) the nucleotide sequence of the cDNA insert of clone CJ397\_1 deposited with the ATCC under accession number 98264;
- 10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

15 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:107, SEQ ID NO:108, and SEQ ID NO:110, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:110, but excluding the poly(A) tail at the 3' end of SEQ ID NO:110. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the

20 cDNA sequence of SEQ ID NO:108, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:108 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:108. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611, and extending contiguously from a nucleotide sequence

25 corresponding to the 5' end of said sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 30 (a) the amino acid sequence of SEQ ID NO:109;
- (b) a fragment of the amino acid sequence of SEQ ID NO:109, the fragment comprising eight contiguous amino acids of SEQ ID NO:109; and
- (c) the amino acid sequence encoded by the cDNA insert of clone CJ397\_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:109. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment preferably comprising eight (more preferably  
5 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:109, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:109.

In one embodiment, the present invention provides a composition comprising an isolated  
10 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111  
15 from nucleotide 204 to nucleotide 1532;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AM795\_4 deposited with the ATCC under accession  
20 number 98271;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AM795\_4 deposited with the ATCC under accession number  
25 98271;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino  
30 acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532; the nucleotide sequence of SEQ ID NO:111 from  
10 nucleotide 204 to nucleotide 1532; the nucleotide sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476; the nucleotide sequence of the full-length protein coding sequence of clone AM795\_4 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone AM795\_4 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a  
15 mature protein encoded by the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112 from amino acid 1 to amino acid 112. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
20 ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 227 to amino acid 236 of SEQ ID NO:112.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

- (ab) the nucleotide sequence of the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and
- (bb) the nucleotide sequence of the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide
- 20 sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111
- 25 from nucleotide 141 to nucleotide 1532, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of
- 30 SEQ ID NO:111 from nucleotide 204 to nucleotide 1532, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 204 to nucleotide 1532, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 204 to nucleotide 1532. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
- 35 corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476,

and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) the amino acid sequence of SEQ ID NO:112 from amino acid 1 to amino acid 112;
- 10 (c) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein  
15 comprises the amino acid sequence of SEQ ID NO:112 or the amino acid sequence of SEQ ID NO:112 from amino acid 1 to amino acid 112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein  
20 comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 227 to amino acid 236 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:114;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AT340\_1 deposited with the ATCC under accession number 98271;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AT340\_1 deposited with the ATCC under accession number 98271;
- 5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:115;
- 10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:115;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:114.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262; the nucleotide sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262; the nucleotide sequence of the full-length protein coding sequence of clone AT340\_1 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone AT340\_1 deposited with the ATCC under accession
- 25 number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:115 from amino acid 1 to amino acid 66. In further preferred embodiments, the present invention provides
- 30 a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:115, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino
- 35 acid 44 of SEQ ID NO:115.



Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:114 and SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 10 (aa) SEQ ID NO:113;
- (ab) SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114; and
- (ac) the nucleotide sequence of the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;
- 15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- 20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:113;
- (bb) SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114; and
- 25 (bc) the nucleotide sequence of the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 30 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:113 and SEQ ID NO:114, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114. Also preferably the polynucleotide isolated

35

according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:114, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:114 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:115;
  - (b) the amino acid sequence of SEQ ID NO:115 from amino acid 1 to amino acid 66;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:115, the fragment comprising eight contiguous amino acids of SEQ ID NO:115; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:115 or the amino acid sequence of SEQ ID NO:115 from amino acid 1 to amino acid 66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:115, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:115.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:116;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG132\_1 deposited with the ATCC under accession number 98271;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG132\_1 deposited with the ATCC under accession number 98271;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:117;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:117;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:116.
- 30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601; the nucleotide sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601; the nucleotide sequence of the full-length protein coding sequence of clone BG132\_1 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone BG132\_1 deposited with the ATCC under accession
- 35 number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a

mature protein encoded by the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:117 from amino acid 119 to amino acid 200. In further preferred embodiments, the present invention  
5 provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:117, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment comprising the amino acid sequence from amino  
10 acid 95 to amino acid 104 of SEQ ID NO:117.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:116 and SEQ ID NO:118.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:116;
- 20 (ab) SEQ ID NO:118, but excluding the poly(A) tail at the 3' end of SEQ ID NO:118; and
- (ac) the nucleotide sequence of the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions  
25 at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in  
30 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:116;
- (bb) SEQ ID NO:118, but excluding the poly(A) tail at the 3' end of SEQ ID NO:118; and

(bc) the nucleotide sequence of the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:116 and SEQ ID NO:118, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID  
10 NO:116 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:118, but excluding the poly(A) tail at the 3' end of SEQ ID NO:118. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:116, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:116 to a nucleotide sequence corresponding to the 3'  
15 end of SEQ ID NO:116. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:116  
20 from nucleotide 2 to nucleotide 601. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ  
25 ID NO:116 from nucleotide 401 to nucleotide 601.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:117;
- (b) the amino acid sequence of SEQ ID NO:117 from amino acid 119 to  
30 amino acid 200;
- (c) a fragment of the amino acid sequence of SEQ ID NO:117, the fragment comprising eight contiguous amino acids of SEQ ID NO:117; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:117 or the amino acid sequence of SEQ ID NO:117 from amino acid 119 to amino acid 200. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:117, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment comprising the amino acid sequence from amino acid 95 to amino acid 104 of SEQ ID NO:117.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG219\_2 deposited with the ATCC under accession number 98271;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG219\_2 deposited with the ATCC under accession number 98271;
- 20 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG219\_2 deposited with the ATCC under accession number 98271;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG219\_2 deposited with the ATCC under accession number 98271;
- 25 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:120;
- 30 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of
- 35 the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:119.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:119  
5 from nucleotide 225 to nucleotide 701; the nucleotide sequence of the full-length protein coding sequence of clone BG219\_2 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone BG219\_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG219\_2  
10 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120 from amino acid 1 to amino acid 97. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment  
15 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:120.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
20 NO:119.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X  
25 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and
    - (ab) the nucleotide sequence of the cDNA insert of clone  
30 BG219\_2 deposited with the ATCC under accession number 98271;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- 35 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and

(bb) the nucleotide sequence of the cDNA insert of clone BG219\_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:119 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide  
20 701, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:120;  
25 (b) the amino acid sequence of SEQ ID NO:120 from amino acid 1 to amino acid 97;

(c) a fragment of the amino acid sequence of SEQ ID NO:120, the fragment comprising eight contiguous amino acids of SEQ ID NO:120; and

(d) the amino acid sequence encoded by the cDNA insert of clone BG219\_2  
30 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:120 or the amino acid sequence of SEQ ID NO:120 from amino acid 1 to amino acid 97. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID  
35 NO:120 having biological activity, the fragment preferably comprising eight (more preferably



twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:120.

- 5           In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:
- (a)   a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121;
  - (b)   a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121  
from nucleotide 2115 to nucleotide 2510;
  - 10       (c)   a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121  
from nucleotide 1 to nucleotide 324;
  - (d)   a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone BG366\_2 deposited with the ATCC under accession  
number 98271;
  - 15       (e)   a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone BG366\_2 deposited with the ATCC under accession number 98271;
  - (f)   a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone BG366\_2 deposited with the ATCC under accession number  
98271;
  - 20       (g)   a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone BG366\_2 deposited with the ATCC under accession number 98271;
  - (h)   a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:122;
  - (i)   a polynucleotide encoding a protein comprising a fragment of the amino  
25       acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising  
eight contiguous amino acids of SEQ ID NO:122;
  - (j)   a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g)  
above;
  - (k)   a polynucleotide which encodes a species homologue of the protein of (h)  
30       or (i) above ;
  - (l)   a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(i); and
  - (m)   a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the  
35       length of SEQ ID NO:121.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510; the nucleotide sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324; the nucleotide sequence of the full-length protein coding sequence of clone BG366\_2 deposited with the ATCC under accession number 98271; or the nucleotide  
5 sequence of a mature protein coding sequence of clone BG366\_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG366\_2 deposited with the ATCC under accession number 98271. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence  
10 of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:122.

15 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:121.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 20 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and
    - 25 (ab) the nucleotide sequence of the cDNA insert of clone BG366\_2 deposited with the ATCC under accession number 98271;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
  - 30 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

(bb) the nucleotide sequence of the cDNA insert of clone BG366\_2 deposited with the ATCC under accession number 98271;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
10 sequence corresponding to the cDNA sequence of SEQ ID NO:121, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:121 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121  
15 from nucleotide 2115 to nucleotide 2510, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA  
20 sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324.

In other embodiments, the present invention provides a composition comprising a protein,  
25 wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:122;

(b) a fragment of the amino acid sequence of SEQ ID NO:122, the fragment comprising eight contiguous amino acids of SEQ ID NO:122; and

(c) the amino acid sequence encoded by the cDNA insert of clone BG366\_2  
30 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:122. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably  
35 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:122.

- In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:
- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123  
10 from nucleotide 27 to nucleotide 181;
  - (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV172\_2 deposited with the ATCC under accession number 98271;
  - (e) a polynucleotide encoding the full-length protein encoded by the cDNA  
15 insert of clone BV172\_2 deposited with the ATCC under accession number 98271;
  - (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV172\_2 deposited with the ATCC under accession number 98271;
  - (g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
20 of clone BV172\_2 deposited with the ATCC under accession number 98271;
  - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:124;
  - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising  
25 eight contiguous amino acids of SEQ ID NO:124;
  - (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
  - (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
  - 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
  - (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:123.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215; the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181; the nucleotide sequence of the full-length protein coding sequence of clone BV172\_2 deposited with the ATCC under accession number 98271; or the  
5 nucleotide sequence of a mature protein coding sequence of clone BV172\_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV172\_2 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid  
10 sequence of SEQ ID NO:124 from amino acid 1 to amino acid 51. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a polynucleotide encoding a protein comprising a fragment of the  
15 amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:124.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:123.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:  
25
      - (aa) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and
      - (ab) the nucleotide sequence of the cDNA insert of clone BV172\_2 deposited with the ATCC under accession number 98271;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions  
30 at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and

(bb) the nucleotide sequence of the cDNA insert of clone BV172\_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:123 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:124;

(b) the amino acid sequence of SEQ ID NO:124 from amino acid 1 to amino acid 51;

(c) a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124; and

(d) the amino acid sequence encoded by the cDNA insert of clone BV172\_2 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:124 or the amino acid sequence of SEQ ID NO:124 from amino acid 1 to amino acid 51. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:124.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CC247\_10 deposited with the ATCC under accession number 98271;
- 20 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CC247\_10 deposited with the ATCC under accession number 98271;
- 25 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:126;
- 30 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:126;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)
- 35 above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:125.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409; the nucleotide sequence of SEQ ID NO:125 from  
10 nucleotide 362 to nucleotide 409; the nucleotide sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419; the nucleotide sequence of the full-length protein coding sequence of clone CC247\_10 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CC247\_10 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-  
15 length or a mature protein encoded by the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a  
20 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 7 to amino acid 16 of SEQ ID NO:126.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:125.

25 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting  
30 of:

(aa) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(ab) the nucleotide sequence of the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;



(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

5 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(bb) the nucleotide sequence of the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:125 to a nucleotide  
20 sequence corresponding to the 3' end of SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide  
25 409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from nucleotide 362  
30 to nucleotide 409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from

nucleotide 270 to nucleotide 419, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 5                   (a)     the amino acid sequence of SEQ ID NO:126;
- (b)     a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126; and
- (c)     the amino acid sequence encoded by the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;
- 10   the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:126. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a protein
- 15   comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 7 to amino acid 16 of SEQ ID NO:126.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 20                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600;
- 25                   (d)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373;
- (e)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CI480\_9 deposited with the ATCC under accession number 98271;
- 30                   (f)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CI480\_9 deposited with the ATCC under accession number 98271;
- (g)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CI480\_9 deposited with the ATCC under accession number 98271;

- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CI480\_9 deposited with the ATCC under accession number 98271;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128;
- 5 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:128;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 10 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of  
15 the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:127.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600; the nucleotide sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600; the nucleotide sequence of SEQ ID NO:127 from nucleotide  
20 62 to nucleotide 373; the nucleotide sequence of the full-length protein coding sequence of clone CI480\_9 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CI480\_9 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CI480\_9 deposited with the ATCC under  
25 accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128 from amino acid 1 to amino acid 82. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably  
30 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:128.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
35 NO:127.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X

5 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and

10 (ab) the nucleotide sequence of the cDNA insert of clone CI480\_9 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

15 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and

(bb) the nucleotide sequence of the cDNA insert of clone CI480\_9 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:127 to a nucleotide  
30 sequence corresponding to the 3' end of SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide  
35 1600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127

from nucleotide 128 to nucleotide 1600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:128;
- (b) the amino acid sequence of SEQ ID NO:128 from amino acid 1 to amino acid 82;
- (c) a fragment of the amino acid sequence of SEQ ID NO:128, the fragment comprising eight contiguous amino acids of SEQ ID NO:128; and
- (d) the amino acid sequence encoded by the cDNA insert of clone C1480\_9 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:128 or the amino acid sequence of SEQ ID NO:128 from amino acid 1 to amino acid 82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:128.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488;
- 5 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
- 10 (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
- 15 (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;
- 20 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- 25 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:129.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958; the nucleotide sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958; the nucleotide sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488; the nucleotide sequence of the full-length protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a

30

35

mature protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34. In further preferred embodiments, the present invention provides  
5 a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 591 to  
10 amino acid 600 of SEQ ID NO:130.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:129.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:129, but excluding the poly(A) tail at the 3'  
20 end of SEQ ID NO:129; and
    - (ab) the nucleotide sequence of the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
30 consisting of:
    - (ba) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and
    - (bb) the nucleotide sequence of the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:129 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129. Also preferably the polynucleotide isolated according to the above  
10 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958. Also preferably the polynucleotide isolated according  
15 to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958. Also preferably the  
20 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide  
25 488.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:130;
- (b) the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino  
30 acid 34;
- (c) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;



the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:130 or the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 591 to amino acid 600 of SEQ ID NO:130.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CT748\_2 deposited with the ATCC under accession number 98271;
- 20 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT748\_2 deposited with the ATCC under accession number 98271;
- 25 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132;
- 30 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:132;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)
- 35 above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:131.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353; the nucleotide sequence of SEQ ID NO:131 from  
10 nucleotide 1793 to nucleotide 2353; the nucleotide sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260; the nucleotide sequence of the full-length protein coding sequence of clone CT748\_2 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CT748\_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-  
15 length or a mature protein encoded by the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132 from amino acid 22 to amino acid 116. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid  
20 sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 234 to amino acid 243 of SEQ ID NO:132.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:131.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

-163-

- (ab) the nucleotide sequence of the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 10 consisting of:
- (ba) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and
- (bb) the nucleotide sequence of the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide
- 20 sequence corresponding to the cDNA sequence of SEQ ID NO:131, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:131 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131
- 25 from nucleotide 914 to nucleotide 2353, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of
- 30 SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
- 35 corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide

1260, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:132;
- (b) the amino acid sequence of SEQ ID NO:132 from amino acid 22 to amino acid 116;
- 10 (c) a fragment of the amino acid sequence of SEQ ID NO:132, the fragment comprising eight contiguous amino acids of SEQ ID NO:132; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein  
1.5 comprises the amino acid sequence of SEQ ID NO:132 or the amino acid sequence of SEQ ID NO:132 from amino acid 22 to amino acid 116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a protein  
20 comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 234 to amino acid 243 of SEQ ID NO:132.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AJ1\_1 deposited with the ATCC under accession  
30 number 98278;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AJ1\_1 deposited with the ATCC under accession number  
35 98278;

- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:134;
- 5 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:134;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 10 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of
- 15 the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:133.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462; the nucleotide sequence of the full-length protein coding sequence of clone AJ1\_1 deposited with the ATCC under accession number 98278; or the

20 nucleotide sequence of a mature protein coding sequence of clone AJ1\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of

25 SEQ ID NO:134 from amino acid 52 to amino acid 147. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a polynucleotide encoding a protein comprising a fragment of the amino acid

30 sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 68 to amino acid 77 of SEQ ID NO:134.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:133 and SEQ ID NO:135.

Further embodiments of the invention provide isolated polynucleotides produced

35 according to a process selected from the group consisting of:

-166-

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (aa) SEQ ID NO:133;
- (ab) SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135; and
- (ac) the nucleotide sequence of the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;
- 10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- 15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:133;
- (bb) SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135; and
- 20 (bc) the nucleotide sequence of the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 25 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:133 and SEQ ID NO:135, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID

30 NO:133 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:133 to a nucleotide sequence corresponding to the 3'

35 end of SEQ ID NO:133. Also preferably the polynucleotide isolated according to the above

process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:134;
- (b) the amino acid sequence of SEQ ID NO:134 from amino acid 52 to amino acid 147;
- (c) a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:134 or the amino acid sequence of SEQ ID NO:134 from amino acid 52 to amino acid 147. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 68 to amino acid 77 of SEQ ID NO:134.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:136;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AQ73\_3 deposited with the ATCC under accession number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AQ73\_3 deposited with the ATCC under accession number 98278;
- 5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:137;
- 10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:137;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:136.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647; the nucleotide sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305; the nucleotide sequence of the full-length protein coding sequence of clone AQ73\_3 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone AQ73\_3 deposited with the ATCC under
- 25 accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:137 from amino acid 1 to amino acid 68. In further preferred embodiments, the present
- 30 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:137, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment comprising the amino acid sequence from
- 35 amino acid 268 to amino acid 277 of SEQ ID NO:137.



Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:136.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 10 (aa) SEQ ID NO:136, but excluding the poly(A) tail at the 3' end of SEQ ID NO:136; and
    - (ab) the nucleotide sequence of the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 20 (ba) SEQ ID NO:136, but excluding the poly(A) tail at the 3' end of SEQ ID NO:136; and
    - (bb) the nucleotide sequence of the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278;
    - 25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
    - (iii) amplifying human DNA sequences; and
    - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:136, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:136 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:136, but excluding the poly(A) tail at the 3' end of SEQ ID NO:136. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647, and extending contiguously from a nucleotide sequence

corresponding to the 5' end of said sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:137;
- (b) the amino acid sequence of SEQ ID NO:137 from amino acid 1 to amino acid 68;
- (c) a fragment of the amino acid sequence of SEQ ID NO:137, the fragment comprising eight contiguous amino acids of SEQ ID NO:137; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:137 or the amino acid sequence of SEQ ID NO:137 from amino acid 1 to amino acid 68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:137, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment comprising the amino acid sequence from amino acid 268 to amino acid 277 of SEQ ID NO:137.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:138;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG142\_1 deposited with the ATCC under accession number 98278;
- 5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG142\_1 deposited with the ATCC under accession number 98278;
- 10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:139;
- 15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:139;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:138.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757; the nucleotide sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703; the nucleotide sequence of the full-length protein coding sequence of clone BG142\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone BG142\_1 deposited with the
- 30 ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:139 from amino acid 184 to amino acid 214. In further preferred
- 35 embodiments, the present invention provides a polynucleotide encoding a protein comprising a

fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:139, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment comprising the amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:139.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:138.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 15 (aa) SEQ ID NO:138, but excluding the poly(A) tail at the 3' end of SEQ ID NO:138; and
    - (ab) the nucleotide sequence of the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (ba) SEQ ID NO:138, but excluding the poly(A) tail at the 3' end of SEQ ID NO:138; and
    - (bb) the nucleotide sequence of the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;
  - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:138, and extending contiguously

from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:138 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:138, but excluding the poly(A) tail at the 3' end of SEQ ID NO:138. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:139;
- (b) the amino acid sequence of SEQ ID NO:139 from amino acid 184 to amino acid 214;
- (c) a fragment of the amino acid sequence of SEQ ID NO:139, the fragment comprising eight contiguous amino acids of SEQ ID NO:139; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:139 or the amino acid sequence of SEQ ID NO:139 from amino acid 184 to amino acid 214. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:139, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment comprising the amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:139.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:140;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV66\_1 deposited with the ATCC under accession number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV66\_1 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:141;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:141;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:140.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535; the nucleotide sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666; the nucleotide sequence of the full-length protein coding sequence of clone BV66\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone BV66\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV66\_1 deposited with the

30

35

ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:141 from amino acid 1 to amino acid 38. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid  
5 sequence of SEQ ID NO:141 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:141, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment comprising the amino acid sequence from amino acid 17 to amino acid 26 of SEQ ID NO:141.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:140.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:140, but excluding the poly(A) tail at the 3' end of SEQ ID NO:140; and
    - 20 (ab) the nucleotide sequence of the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
  - 25 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 30 (ba) SEQ ID NO:140, but excluding the poly(A) tail at the 3' end of SEQ ID NO:140; and
    - (bb) the nucleotide sequence of the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions
    - 35 at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:140, and extending contiguously  
5 from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:140 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:140, but excluding the poly(A) tail at the 3' end of SEQ ID NO:140. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535, and extending contiguously from a nucleotide sequence  
10 corresponding to the 5' end of said sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666, and extending contiguously from a nucleotide  
15 sequence corresponding to the 5' end of said sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:141;
- (b) the amino acid sequence of SEQ ID NO:141 from amino acid 1 to amino acid 38;
- (c) a fragment of the amino acid sequence of SEQ ID NO:141, the fragment comprising eight contiguous amino acids of SEQ ID NO:141; and
- 25 (d) the amino acid sequence encoded by the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:141 or the amino acid sequence of SEQ ID NO:141 from amino acid 1 to amino acid 38. In further preferred embodiments, the present  
30 invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:141, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment comprising the amino acid sequence from amino acid 17 to amino acid 26 of SEQ  
35 ID NO:141.



In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:142;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:142  
5 from nucleotide 1204 to nucleotide 1389;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:142  
from nucleotide 881 to nucleotide 1380;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone BV291\_3 deposited with the ATCC under accession  
10 number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone BV291\_3 deposited with the ATCC under accession number 98278;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone BV291\_3 deposited with the ATCC under accession number  
15 98278;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone BV291\_3 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:143;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino  
20 acid sequence of SEQ ID NO:143 having biological activity, the fragment comprising  
eight contiguous amino acids of SEQ ID NO:143;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g)  
above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h)  
25 or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the  
length of SEQ ID NO:142.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:142  
from nucleotide 1204 to nucleotide 1389; the nucleotide sequence of SEQ ID NO:142 from  
nucleotide 881 to nucleotide 1380; the nucleotide sequence of the full-length protein coding  
35 sequence of clone BV291\_3 deposited with the ATCC under accession number 98278; or the

nucleotide sequence of a mature protein coding sequence of clone BV291\_3 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV291\_3 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:143 from amino acid 1 to amino acid 59. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:143, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:143.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:142.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:142, but excluding the poly(A) tail at the 3' end of SEQ ID NO:142; and

(ab) the nucleotide sequence of the cDNA insert of clone BV291\_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:142, but excluding the poly(A) tail at the 3' end of SEQ ID NO:142; and

-179-

- (bb) the nucleotide sequence of the cDNA insert of clone BV291\_3 deposited with the ATCC under accession number 98278;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:142, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:142 to a nucleotide

10 sequence corresponding to the 3' end of SEQ ID NO:142, but excluding the poly(A) tail at the 3' end of SEQ ID NO:142. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:142 from nucleotide 1204 to nucleotide 1389, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:142 from nucleotide 1204 to

15 nucleotide 1389, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:142 from nucleotide 1204 to nucleotide 1389. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:142 from nucleotide 881 to nucleotide 1380, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:142 from

20 nucleotide 881 to nucleotide 1380, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:142 from nucleotide 881 to nucleotide 1380.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:143;
- 25 (b) the amino acid sequence of SEQ ID NO:143 from amino acid 1 to amino acid 59;
- (c) a fragment of the amino acid sequence of SEQ ID NO:143, the fragment comprising eight contiguous amino acids of SEQ ID NO:143; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BV291\_3
- 30 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:143 or the amino acid sequence of SEQ ID NO:143 from amino acid 1 to amino acid 59. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID

35 NO:143 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:143, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:143.

- 5           In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:
- (a)   a polynucleotide comprising the nucleotide sequence of SEQ ID NO:144;
  - (b)   a polynucleotide comprising the nucleotide sequence of SEQ ID NO:144  
from nucleotide 189 to nucleotide 1115;
  - 10       (c)   a polynucleotide comprising the nucleotide sequence of SEQ ID NO:144  
from nucleotide 1 to nucleotide 451;
  - (d)   a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone CK201\_1 deposited with the ATCC under accession  
number 98278;
  - 15       (e)   a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone CK201\_1 deposited with the ATCC under accession number 98278;
  - (f)   a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone CK201\_1 deposited with the ATCC under accession number  
98278;
  - 20       (g)   a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone CK201\_1 deposited with the ATCC under accession number 98278;
  - (h)   a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:145;
  - (i)   a polynucleotide encoding a protein comprising a fragment of the amino  
25       acid sequence of SEQ ID NO:145 having biological activity, the fragment comprising  
eight contiguous amino acids of SEQ ID NO:145;
  - (j)   a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g)  
above;
  - (k)   a polynucleotide which encodes a species homologue of the protein of (h)  
30       or (i) above ;
  - (l)   a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(i); and
  - (m)   a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the  
35       length of SEQ ID NO:144.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115; the nucleotide sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451; the nucleotide sequence of the full-length protein coding sequence of clone CK201\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CK201\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CK201\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:145 from amino acid 1 to amino acid 88. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:145, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:145.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:144.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:144, but excluding the poly(A) tail at the 3' end of SEQ ID NO:144; and
    - (ab) the nucleotide sequence of the cDNA insert of clone CK201\_1 deposited with the ATCC under accession number 98278;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

-182-

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:144, but excluding the poly(A) tail at the 3' end of SEQ ID NO:144; and

(bb) the nucleotide sequence of the cDNA insert of clone CK201\_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:144, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:144 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:144, but excluding the poly(A) tail at the 3' end of SEQ ID NO:144. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide  
20 1115, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:144 from  
25 nucleotide 1 to nucleotide 451, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:145;  
30 (b) the amino acid sequence of SEQ ID NO:145 from amino acid 1 to amino acid 88;

(c) a fragment of the amino acid sequence of SEQ ID NO:145, the fragment comprising eight contiguous amino acids of SEQ ID NO:145; and

(d) the amino acid sequence encoded by the cDNA insert of clone CK201\_1  
35 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:145 or the amino acid sequence of SEQ ID NO:145 from amino acid 1 to amino acid 88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:145, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:145.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- 20 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- 25 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:147;
- 30 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:147;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)
- 35 above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:146.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923; the nucleotide sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923; the nucleotide sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316; the nucleotide sequence of the full-length protein coding sequence of clone CQ331\_2 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CQ331\_2 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:147 from amino acid 1 to amino acid 57. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:147, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:147.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:146.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

30 (a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:146, but excluding the poly(A) tail at the 3' end of SEQ ID NO:146; and



- (ab) the nucleotide sequence of the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 10 consisting of:
- (ba) SEQ ID NO:146, but excluding the poly(A) tail at the 3' end of SEQ ID NO:146; and
- (bb) the nucleotide sequence of the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide
- 20 sequence corresponding to the cDNA sequence of SEQ ID NO:146, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:146 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:146, but excluding the poly(A) tail at the 3' end of SEQ ID NO:146. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:146
- 25 from nucleotide 117 to nucleotide 923, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ
- 30 ID NO:146 from nucleotide 174 to nucleotide 923, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA
- 35 sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316, and extending contiguously

from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316.

In other embodiments, the present invention provides a composition comprising a protein,  
5 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:147;
- (b) the amino acid sequence of SEQ ID NO:147 from amino acid 1 to amino acid 57;
- (c) a fragment of the amino acid sequence of SEQ ID NO:147, the fragment  
10 comprising eight contiguous amino acids of SEQ ID NO:147; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:147 or the amino acid sequence of SEQ ID  
15 NO:147 from amino acid 1 to amino acid 57. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:147, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity,  
20 the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:147.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:148;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length  
30 protein coding sequence of clone CT550\_1 deposited with the ATCC under accession number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT550\_1 deposited with the ATCC under accession number 98278;
- 5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:149;
- 10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:149;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:148.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483; the nucleotide sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397; the nucleotide sequence of the full-length protein coding sequence of clone CT550\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CT550\_1 deposited with the
- 25 ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:149 from amino acid 1 to amino acid 58. In further preferred
- 30 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:149, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment comprising the
- 35 amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:149.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:148.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:148, but excluding the poly(A) tail at the 3' end of SEQ ID NO:148; and
- (ab) the nucleotide sequence of the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 20 (ba) SEQ ID NO:148, but excluding the poly(A) tail at the 3' end of SEQ ID NO:148; and
- (bb) the nucleotide sequence of the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;
- 25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:148, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:148 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:148, but excluding the poly(A) tail at the 3' end of SEQ ID NO:148. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483, and extending contiguously from a nucleotide sequence

30

35

corresponding to the 5' end of said sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:149;
- (b) the amino acid sequence of SEQ ID NO:149 from amino acid 1 to amino acid 58;
- (c) a fragment of the amino acid sequence of SEQ ID NO:149, the fragment comprising eight contiguous amino acids of SEQ ID NO:149; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:149 or the amino acid sequence of SEQ ID NO:149 from amino acid 1 to amino acid 58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:149, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:149.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CT585\_1 deposited with the ATCC under accession number 98278;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT585\_1 deposited with the ATCC under accession number 98278;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:151;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment comprising 15 eight contiguous amino acids of SEQ ID NO:151;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:150.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969; the nucleotide sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969; the nucleotide sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423; the nucleotide sequence of the full-length protein coding sequence of clone CT585\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence
- 30 of a mature protein coding sequence of clone CT585\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:151 from
- 35 amino acid 1 to amino acid 104. In further preferred embodiments, the present invention provides

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:151, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having  
5 biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:151.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:150.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:150, but excluding the poly(A) tail at the 3' end of SEQ ID NO:150; and

(ab) the nucleotide sequence of the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
20 at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in  
25 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:150, but excluding the poly(A) tail at the 3' end of SEQ ID NO:150; and

(bb) the nucleotide sequence of the cDNA insert of clone  
30 CT585\_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:150 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:150, but excluding the poly(A) tail at the 3' end of SEQ ID NO:150. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:151;
- (b) the amino acid sequence of SEQ ID NO:151 from amino acid 1 to amino acid 104;
- (c) a fragment of the amino acid sequence of SEQ ID NO:151, the fragment comprising eight contiguous amino acids of SEQ ID NO:151; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:151 or the amino acid sequence of SEQ ID NO:151 from amino acid 1 to amino acid 104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:151, or a protein



comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:151.

In one embodiment, the present invention provides a composition comprising an isolated  
5 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:152;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:152  
10 from nucleotide 243 to nucleotide 789;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CT797\_3 deposited with the ATCC under accession number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA  
15 insert of clone CT797\_3 deposited with the ATCC under accession number 98278;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT797\_3 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
20 of clone CT797\_3 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:153;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment comprising  
25 eight contiguous amino acids of SEQ ID NO:153;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:152.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766; the nucleotide sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789; the nucleotide sequence of the full-length protein coding sequence of clone CT797\_3 deposited with the ATCC under accession number 98278; or the  
5 nucleotide sequence of a mature protein coding sequence of clone CT797\_3 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT797\_3 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid  
10 sequence of SEQ ID NO:153 from amino acid 75 to amino acid 251. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:153, or a polynucleotide encoding a protein comprising a fragment of the  
15 amino acid sequence of SEQ ID NO:153 having biological activity, the fragment comprising the amino acid sequence from amino acid 450 to amino acid 459 of SEQ ID NO:153.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:152.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - 25 (aa) SEQ ID NO:152, but excluding the poly(A) tail at the 3' end of SEQ ID NO:152; and
      - (ab) the nucleotide sequence of the cDNA insert of clone CT797\_3 deposited with the ATCC under accession number 98278;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions  
30 at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

-195-

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:152, but excluding the poly(A) tail at the 3' end of SEQ ID NO:152; and

(bb) the nucleotide sequence of the cDNA insert of clone CT797\_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:152, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:152 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:152, but excluding the poly(A) tail at the 3' end of SEQ ID NO:152. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide  
20 2766, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:152 from nucleotide 243  
25 to nucleotide 789, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:153;  
30 (b) the amino acid sequence of SEQ ID NO:153 from amino acid 75 to amino acid 251;

(c) a fragment of the amino acid sequence of SEQ ID NO:153, the fragment comprising eight contiguous amino acids of SEQ ID NO:153; and

(d) the amino acid sequence encoded by the cDNA insert of clone CT797\_3  
35 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:153 or the amino acid sequence of SEQ ID NO:153 from amino acid 75 to amino acid 251. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:153, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment comprising the amino acid sequence from amino acid 450 to amino acid 459 of SEQ ID NO:153.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CB107\_1 deposited with the ATCC under accession number 98279;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;
- 20 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CB107\_1 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;
- 25 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:156;
- 30 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of
- 35 the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:155.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:155  
5 from nucleotide 41 to nucleotide 760; the nucleotide sequence of the full-length protein coding sequence of clone CB107\_1 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CB107\_1 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CB107\_1  
10 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156 from amino acid 127 to amino acid 240. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment  
15 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:156.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
20 NO:155, SEQ ID NO:154, and SEQ ID NO:157.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X  
25 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:154;
    - (ab) SEQ ID NO:155;
    - (ac) SEQ ID NO:157, but excluding the poly(A) tail at the 3'  
30 end of SEQ ID NO:157; and
    - (ad) the nucleotide sequence of the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);  
35

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:154;

(bb) SEQ ID NO:155;

(bc) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and

(bd) the nucleotide sequence of the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:154, SEQ ID NO:155, and SEQ ID NO:157, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:154 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:155 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:155. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:156;

(b) the amino acid sequence of SEQ ID NO:156 from amino acid 127 to amino acid 240;

(c) a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156; and

(d) the amino acid sequence encoded by the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:156 or the amino acid sequence of SEQ ID NO:156 from amino acid 127 to amino acid 240. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably comprising eight (more preferably  
10 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:156.

In one embodiment, the present invention provides a composition comprising an isolated  
15 polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158  
20 from nucleotide 500 to nucleotide 1108;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CG300\_3 deposited with the ATCC under accession  
25 number 98279;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CG300\_3 deposited with the ATCC under accession number  
30 98279;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:159;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:159;

5 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

10 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:158.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108; the nucleotide sequence of SEQ ID NO:158 from  
15 nucleotide 500 to nucleotide 1108; the nucleotide sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387; the nucleotide sequence of the full-length protein coding sequence of clone CG300\_3 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CG300\_3 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a  
20 mature protein encoded by the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:159 from amino acid 23 to amino acid 57. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
25 ID NO:159 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:159, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:159.

30 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:158.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:



-201-

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:158, but excluding the poly(A) tail at the 3' end of SEQ ID NO:158; and

(ab) the nucleotide sequence of the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:158, but excluding the poly(A) tail at the 3' end of SEQ ID NO:158; and

(bb) the nucleotide sequence of the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;

20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:158, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:158 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:158, but excluding the poly(A) tail at the 3' end of SEQ ID NO:158. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:158

30 from nucleotide 374 to nucleotide 1108, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of

35 SEQ ID NO:158 from nucleotide 500 to nucleotide 1108, and extending contiguously from a

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:158 from nucleotide 500 to nucleotide 1108, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:158 from nucleotide 500 to nucleotide 1108. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387.

In other embodiments, the present invention provides a composition comprising a protein,  
10 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:159;
- (b) the amino acid sequence of SEQ ID NO:159 from amino acid 23 to amino acid 57;
- (c) a fragment of the amino acid sequence of SEQ ID NO:159, the fragment  
15 comprising eight contiguous amino acids of SEQ ID NO:159; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:159 or the amino acid sequence of SEQ ID  
20 NO:159 from amino acid 23 to amino acid 57. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:159, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity,  
25 the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:159.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160;
- 30 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160  
35 from nucleotide 49 to nucleotide 382;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CJ145\_1 deposited with the ATCC under accession number 98279;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CJ145\_1 deposited with the ATCC under accession number 98279;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:161;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment comprising 15 eight contiguous amino acids of SEQ ID NO:161;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:160.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053; the nucleotide sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053; the nucleotide sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382; the nucleotide sequence of the full-length protein coding sequence of clone CJ145\_1 deposited with the ATCC under accession number 98279; or the nucleotide sequence of
- 30 a mature protein coding sequence of clone CJ145\_1 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:161 from
- 35 amino acid 1 to amino acid 87. In further preferred embodiments, the present invention provides

WO 01/19988

PCT/US00/25135

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:161, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment comprising the amino acid sequence from amino acid 482 to amino acid 491 of SEQ ID NO:161.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:160.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:160, but excluding the poly(A) tail at the 3' end of SEQ ID NO:160; and

- (ab) the nucleotide sequence of the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:160, but excluding the poly(A) tail at the 3' end of SEQ ID NO:160; and

- (bb) the nucleotide sequence of the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and

- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:160 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:160, but excluding the poly(A) tail at the 3' end of SEQ ID NO:160. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:161;
- (b) the amino acid sequence of SEQ ID NO:161 from amino acid 1 to amino acid 87;
- (c) a fragment of the amino acid sequence of SEQ ID NO:161, the fragment comprising eight contiguous amino acids of SEQ ID NO:161; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:161 or the amino acid sequence of SEQ ID NO:161 from amino acid 1 to amino acid 87. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:161, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment comprising the amino acid sequence from amino acid 482 to amino acid 491 of SEQ ID NO:161.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162  
from nucleotide 40 to nucleotide 342;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162  
from nucleotide 127 to nucleotide 342;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162  
from nucleotide 11 to nucleotide 181;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length  
15 protein coding sequence of clone CJ160\_11 deposited with the ATCC under accession  
number 98279;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein  
20 coding sequence of clone CJ160\_11 deposited with the ATCC under accession number  
98279;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence  
25 of SEQ ID NO:163;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:163 having biological activity, the fragment comprising  
eight contiguous amino acids of SEQ ID NO:163;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)  
30 above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i)  
or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:162.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342; the nucleotide sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342; the nucleotide sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181; the nucleotide sequence of the full-length protein coding sequence of clone CJ160\_11 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CJ160\_11 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:163 from amino acid 7 to amino acid 48. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:163, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:163.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:162.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 25 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 30 (aa) SEQ ID NO:162, but excluding the poly(A) tail at the 3' end of SEQ ID NO:162; and
    - (ab) the nucleotide sequence of the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 35 (iii) isolating the DNA polynucleotides detected with the probe(s);



and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:162, but excluding the poly(A) tail at the 3' end of SEQ ID NO:162; and
- (bb) the nucleotide sequence of the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:162 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:162, but excluding the poly(A) tail at the 3' end of SEQ ID NO:162. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:163;
- (b) the amino acid sequence of SEQ ID NO:163 from amino acid 7 to amino acid 48;
- (c) a fragment of the amino acid sequence of SEQ ID NO:163, the fragment comprising eight contiguous amino acids of SEQ ID NO:163; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:163 or the amino acid sequence of SEQ ID NO:163 from amino acid 7 to amino acid 48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:163, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:163.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:164;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO20\_1 deposited with the ATCC under accession number 98279;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO20\_1 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:165;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:165;
- 5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:164.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467; the nucleotide sequence of SEQ ID NO:164 from  
15 nucleotide 267 to nucleotide 467; the nucleotide sequence of the full-length protein coding sequence of clone CO20\_1 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CO20\_1 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO20\_1  
20 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:165 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment  
25 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:165, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:165.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
30 NO:164 and SEQ ID NO:166.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:164;

(ab) SEQ ID NO:166, but excluding the poly(A) tail at the 3' end of SEQ ID NO:166; and

(ac) the nucleotide sequence of the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:164;

(bb) SEQ ID NO:166, but excluding the poly(A) tail at the 3' end of SEQ ID NO:166; and

(bc) the nucleotide sequence of the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:164 and SEQ ID NO:166, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:164 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:166, but excluding the poly(A) tail at the 3' end of SEQ ID NO:166. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:164, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:164 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:164. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:164

from nucleotide 180 to nucleotide 467, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:165;
- (b) the amino acid sequence of SEQ ID NO:165 from amino acid 1 to amino acid 37;
- 15 (c) a fragment of the amino acid sequence of SEQ ID NO:165, the fragment comprising eight contiguous amino acids of SEQ ID NO:165; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:165 or the amino acid sequence of SEQ ID NO:165 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:165, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:165.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520;

- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO223\_3 deposited with the ATCC under accession number 98291;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO223\_3 deposited with the ATCC under accession number 98291;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO223\_3 deposited with the ATCC under accession number 98291;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO223\_3 deposited with the ATCC under accession number 98291;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:168;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:168;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:167.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520; the nucleotide sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520; the nucleotide sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413; the nucleotide sequence of the full-length protein coding sequence of clone CO223\_3 deposited with the ATCC under accession number 98291; or the nucleotide sequence of a mature protein coding sequence of clone CO223\_3 deposited with the ATCC under accession number 98291. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO223\_3 deposited with the ATCC under accession number 98291. In yet other preferred embodiments, the present invention provides a

polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:168 from amino acid 1 to amino acid 80. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably  
5 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:168, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:168.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
10 NO:167.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X  
15 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167; and

(ab) the nucleotide sequence of the cDNA insert of clone  
20 CO223\_3 deposited with the ATCC under accession number 98291;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:  
(i) preparing one or more polynucleotide primers that hybridize in  
25 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167; and

(bb) the nucleotide sequence of the cDNA insert of clone  
30 CO223\_3 deposited with the ATCC under accession number 98291;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and  
35

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:167 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:168;
- (b) the amino acid sequence of SEQ ID NO:168 from amino acid 1 to amino acid 80;
- (c) a fragment of the amino acid sequence of SEQ ID NO:168, the fragment comprising eight contiguous amino acids of SEQ ID NO:168; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CO223\_3 deposited with the ATCC under accession number 98291;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:168 or the amino acid sequence of SEQ ID NO:168 from amino acid 1 to amino acid 80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably



twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:168, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:168.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO310\_2 deposited with the ATCC under accession number 98279;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO310\_2 deposited with the ATCC under accession number 98279;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:170;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:170;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:169.
- 35

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542; the nucleotide sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435; the nucleotide sequence of the full-length protein coding sequence of clone CO310\_2 deposited with the ATCC under accession number 98279; or the nucleotide  
5 sequence of a mature protein coding sequence of clone CO310\_2 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID  
10 NO:170 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:170, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
15 ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:170.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:169.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (aa) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and

(ab) the nucleotide sequence of the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
30 at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and

(bb) the nucleotide sequence of the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:169 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide  
20 542, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:169 from nucleotide 1 to  
25 nucleotide 435, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:170;  
30 (b) the amino acid sequence of SEQ ID NO:170 from amino acid 1 to amino acid 44;

(c) a fragment of the amino acid sequence of SEQ ID NO:170, the fragment comprising eight contiguous amino acids of SEQ ID NO:170; and

(d) the amino acid sequence encoded by the cDNA insert of clone CO310\_2  
35 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:170 or the amino acid sequence of SEQ ID NO:170 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:170, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:170.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CP258\_3 deposited with the ATCC under accession number 98279;
- 20 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CP258\_3 deposited with the ATCC under accession number 98279;
- 25 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:172;
- 30 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:172;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 35

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:171.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455; the nucleotide sequence of SEQ ID NO:171 from nucleotide  
10 85 to nucleotide 455; the nucleotide sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515; the nucleotide sequence of the full-length protein coding sequence of clone CP258\_3 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CP258\_3 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a  
15 mature protein encoded by the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:172 from amino acid 64 to amino acid 138. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence  
20 of SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:172, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:172.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:171.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171; and

- (ab) the nucleotide sequence of the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 10 consisting of:
- (ba) SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171; and
- (bb) the nucleotide sequence of the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide
- 20 sequence corresponding to the cDNA sequence of SEQ ID NO:171, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:171 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:171
- 25 from nucleotide 40 to nucleotide 455, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ
- 30 ID NO:171 from nucleotide 85 to nucleotide 455, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA
- 35 sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515, and extending contiguously

from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515.

In other embodiments, the present invention provides a composition comprising a protein,  
5 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:172;
- (b) the amino acid sequence of SEQ ID NO:172 from amino acid 64 to amino acid 138;
- (c) a fragment of the amino acid sequence of SEQ ID NO:172, the fragment  
10 comprising eight contiguous amino acids of SEQ ID NO:172; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:172 or the amino acid sequence of SEQ ID  
15 NO:172 from amino acid 64 to amino acid 138. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:172, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity,  
20 the fragment comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:172.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173  
30 from nucleotide 1 to nucleotide 352;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW1155\_3 deposited with the ATCC under accession number 98279;
- 35 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279;

- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW1155\_3 deposited with the ATCC under accession number 98279;
- 5 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:174;
- 10 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:174;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:173.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007; the nucleotide sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007; the nucleotide sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352; the nucleotide sequence of the full-length protein coding sequence of clone CW1155\_3 deposited with the ATCC under accession number 98279; or the nucleotide sequence
- 25 of a mature protein coding sequence of clone CW1155\_3 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID
- 30 NO:174 from amino acid 1 to amino acid 83. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ



ID NO:174 having biological activity, the fragment comprising the amino acid sequence from amino acid 145 to amino acid 154 of SEQ ID NO:174.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:173.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X  
10 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:173, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:173; and

(ab) the nucleotide sequence of the cDNA insert of clone  
CW1155\_3 deposited with the ATCC under accession number 98279;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:173, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:173; and

25 (bb) the nucleotide sequence of the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

30 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:173 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:173, but excluding the poly(A) tail at the 3'  
35 end of SEQ ID NO:173. Also preferably the polynucleotide isolated according to the above

process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:174;
  - (b) the amino acid sequence of SEQ ID NO:174 from amino acid 1 to amino acid 83;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:174, the fragment comprising eight contiguous amino acids of SEQ ID NO:174; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:174 or the amino acid sequence of SEQ ID NO:174 from amino acid 1 to amino acid 83. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising the amino acid sequence from amino acid 145 to amino acid 154 of SEQ ID NO:174.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134;
- 10 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CZ247\_2 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CZ247\_2 deposited with the ATCC under accession number 15 98279;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:176;
- 20 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:176;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 25 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- 30 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:175.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699; the nucleotide sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699; the nucleotide sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134; the nucleotide sequence of the full-length protein coding sequence of
- 35

clone CZ247\_2 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CZ247\_2 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:176 from amino acid 298 to amino acid 374. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:176, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising the amino acid sequence from amino acid 276 to amino acid 285 of SEQ ID NO:176.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:175.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175; and
      - (ab) the nucleotide sequence of the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175; and

- (bb) the nucleotide sequence of the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:175 to a nucleotide  
10 sequence corresponding to the 3' end of SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide  
15 1699, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from  
20 nucleotide 1682 to nucleotide 1699, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said  
25 sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 30 (a) the amino acid sequence of SEQ ID NO:176;
- (b) the amino acid sequence of SEQ ID NO:176 from amino acid 298 to amino acid 374;
- (c) a fragment of the amino acid sequence of SEQ ID NO:176, the fragment comprising eight contiguous amino acids of SEQ ID NO:176; and

(d) the amino acid sequence encoded by the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:176 or the amino acid sequence of SEQ ID NO:176 from amino acid 298 to amino acid 374. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:176, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising the amino acid sequence from amino acid 276 to amino acid 285 of SEQ ID NO:176.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AM666\_1 deposited with the ATCC under accession number 98292;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AM666\_1 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:178;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:178;

- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:177.
- 10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262; the nucleotide sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262; the nucleotide sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134; the nucleotide sequence of the full-length protein coding sequence of clone AM666\_1 deposited with the ATCC under accession number 98292; or the nucleotide
- 15 sequence of a mature protein coding sequence of clone AM666\_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID
- 20 NO:178 from amino acid 5 to amino acid 72. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:178, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ
- 25 ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:178.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:177.

Further embodiments of the invention provide isolated polynucleotides produced

30 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

-231-

- (aa) SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177; and
- (ab) the nucleotide sequence of the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292;
- 5 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- 10 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177; and
- 15 (bb) the nucleotide sequence of the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- 20 (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:177 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262. Also preferably the
- 35



polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:178;
- 10 (b) the amino acid sequence of SEQ ID NO:178 from amino acid 5 to amino acid 72;
- (c) a fragment of the amino acid sequence of SEQ ID NO:178, the fragment comprising eight contiguous amino acids of SEQ ID NO:178; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AM666\_1
- 15 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:178 or the amino acid sequence of SEQ ID NO:178 from amino acid 5 to amino acid 72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:178, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:178.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906;
- 30 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BN387\_3 deposited with the ATCC under accession number 98292;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BN387\_3 deposited with the ATCC under accession number 98292;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:180;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising 15 eight contiguous amino acids of SEQ ID NO:180;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:179.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906; the nucleotide sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906; the nucleotide sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831; the nucleotide sequence of the full-length protein coding sequence of clone BN387\_3 deposited with the ATCC under accession number 98292; or the nucleotide sequence
- 30 of a mature protein coding sequence of clone BN387\_3 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:180 from
- 35 amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:180, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having  
5 biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:180.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:179.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and

(ab) the nucleotide sequence of the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and

30 (bb) the nucleotide sequence of the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:179 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:180;
  - (b) the amino acid sequence of SEQ ID NO:180 from amino acid 1 to amino acid 27;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:180, the fragment comprising eight contiguous amino acids of SEQ ID NO:180; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:180 or the amino acid sequence of SEQ ID NO:180 from amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:180, or a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:180.

- In one embodiment, the present invention provides a composition comprising an isolated
- 5 polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181  
10 from nucleotide 1 to nucleotide 416;
  - (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BQ135\_2 deposited with the ATCC under accession number 98292;
  - (e) a polynucleotide encoding the full-length protein encoded by the cDNA  
15 insert of clone BQ135\_2 deposited with the ATCC under accession number 98292;
  - (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BQ135\_2 deposited with the ATCC under accession number 98292;
  - (g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
20 of clone BQ135\_2 deposited with the ATCC under accession number 98292;
  - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:182;
  - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising  
25 eight contiguous amino acids of SEQ ID NO:182;
  - (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
  - (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
  - (l) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(i); and
  - (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:181.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765; the nucleotide sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416; the nucleotide sequence of the full-length protein coding sequence of clone BQ135\_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone BQ135\_2 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BQ135\_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:182 from amino acid 1 to amino acid 93. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:182.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:181.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and
    - (ab) the nucleotide sequence of the cDNA insert of clone BQ135\_2 deposited with the ATCC under accession number 98292;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and

(bb) the nucleotide sequence of the cDNA insert of clone BQ135\_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:181 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide  
20 765, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from nucleotide 1 to  
25 nucleotide 416, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:182;  
30 (b) the amino acid sequence of SEQ ID NO:182 from amino acid 1 to amino acid 93;

(c) a fragment of the amino acid sequence of SEQ ID NO:182, the fragment comprising eight contiguous amino acids of SEQ ID NO:182; and

(d) the amino acid sequence encoded by the cDNA insert of clone BQ135\_2  
35 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:182 or the amino acid sequence of SEQ ID NO:182 from amino acid 1 to amino acid 93. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID  
5 NO:182 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:182.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CR678\_1 deposited with the ATCC under accession number 98292;
- 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CR678\_1 deposited with the ATCC under accession number 98292;
- 25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:184;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino  
30 acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:184;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h)  
35 or (i) above ;



(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:183.

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714; the nucleotide sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531; the nucleotide sequence of the full-length protein coding sequence of clone CR678\_1 deposited with the ATCC under accession number 98292; or the  
10 nucleotide sequence of a mature protein coding sequence of clone CR678\_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid  
15 sequence of SEQ ID NO:184 from amino acid 1 to amino acid 106. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:184, or a polynucleotide encoding a protein comprising a fragment of the  
20 amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:184.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:183.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183; and

(ab) the nucleotide sequence of the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
35 at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in  
5 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
consisting of:

(ba) SEQ ID NO:183, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:183; and

(bb) the nucleotide sequence of the cDNA insert of clone  
10 CR678\_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

15 Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
sequence corresponding to the cDNA sequence of SEQ ID NO:183, and extending contiguously  
from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:183 to a nucleotide  
sequence corresponding to the 3' end of SEQ ID NO:183, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:183. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183  
from nucleotide 214 to nucleotide 714, and extending contiguously from a nucleotide sequence  
corresponding to the 5' end of said sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide  
714, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:183  
from nucleotide 214 to nucleotide 714. Also preferably the polynucleotide isolated according to  
25 the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ  
ID NO:183 from nucleotide 151 to nucleotide 531, and extending contiguously from a nucleotide  
sequence corresponding to the 5' end of said sequence of SEQ ID NO:183 from nucleotide 151  
to nucleotide 531, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ  
ID NO:183 from nucleotide 151 to nucleotide 531.

30 In other embodiments, the present invention provides a composition comprising a protein,  
wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:184;

(b) the amino acid sequence of SEQ ID NO:184 from amino acid 1 to amino  
acid 106;

(c) a fragment of the amino acid sequence of SEQ ID NO:184, the fragment comprising eight contiguous amino acids of SEQ ID NO:184; and

(d) the amino acid sequence encoded by the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:184 or the amino acid sequence of SEQ ID NO:184 from amino acid 1 to amino acid 106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight (more preferably  
10 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:184, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:184.

In one embodiment, the present invention provides a composition comprising an isolated  
15 polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185  
20 from nucleotide 1221 to nucleotide 1711;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW420\_2 deposited with the ATCC under accession number 98292;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA  
25 insert of clone CW420\_2 deposited with the ATCC under accession number 98292;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW420\_2 deposited with the ATCC under accession number 98292;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
30 of clone CW420\_2 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:186;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising  
35 eight contiguous amino acids of SEQ ID NO:186;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:185.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498; the nucleotide sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711; the nucleotide sequence of the full-length protein coding sequence of clone CW420\_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CW420\_2 deposited with the  
15 ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW420\_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:186 from amino acid 370 to amino acid 532. In further preferred  
20 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:186, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising the  
25 amino acid sequence from amino acid 725 to amino acid 734 of SEQ ID NO:186.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:185.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

30 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:185, but excluding the poly(A) tail at the 3'  
35 end of SEQ ID NO:185; and

- (ab) the nucleotide sequence of the cDNA insert of clone CW420\_2 deposited with the ATCC under accession number 98292;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 10 consisting of:
- (ba) SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185; and
- (bb) the nucleotide sequence of the cDNA insert of clone CW420\_2 deposited with the ATCC under accession number 98292;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide

20 sequence corresponding to the cDNA sequence of SEQ ID NO:185, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:185 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185

25 from nucleotide 116 to nucleotide 4498, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of

30 SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711.

In other embodiments, the present invention provides a composition comprising a protein,

35 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:186;
- (b) the amino acid sequence of SEQ ID NO:186 from amino acid 370 to amino acid 532;
- (c) a fragment of the amino acid sequence of SEQ ID NO:186, the fragment comprising eight contiguous amino acids of SEQ ID NO:186; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CW420\_2 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:186 or the amino acid sequence of SEQ ID NO:186 from amino acid 370 to amino acid 532. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:186, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising the amino acid sequence from amino acid 725 to amino acid 734 of SEQ ID NO:186.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW795\_2 deposited with the ATCC under accession number 98292;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW795\_2 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:188;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:188;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:187.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176; the nucleotide sequence of SEQ ID NO:187 from  
15 nucleotide 1 to nucleotide 529; the nucleotide sequence of the full-length protein coding sequence of clone CW795\_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CW795\_2 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW795\_2 deposited with the  
20 ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:188 from amino acid 1 to amino acid 137. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment preferably comprising eight  
25 (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:188, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising the amino acid sequence from amino acid 338 to amino acid 347 of SEQ ID NO:188.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
30 NO:187.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187; and

(ab) the nucleotide sequence of the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187; and

(bb) the nucleotide sequence of the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;

20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
25 sequence corresponding to the cDNA sequence of SEQ ID NO:187, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:187 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187  
30 from nucleotide 119 to nucleotide 2176, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of  
35 SEQ ID NO:187 from nucleotide 1 to nucleotide 529, and extending contiguously from a



nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529.

In other embodiments, the present invention provides a composition comprising a protein,  
5 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:188;
- (b) the amino acid sequence of SEQ ID NO:188 from amino acid 1 to amino acid 137;
- (c) a fragment of the amino acid sequence of SEQ ID NO:188, the fragment  
10 comprising eight contiguous amino acids of SEQ ID NO:188; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:188 or the amino acid sequence of SEQ ID  
15 NO:188 from amino acid 1 to amino acid 137. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:188, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity,  
20 the fragment comprising the amino acid sequence from amino acid 338 to amino acid 347 of SEQ ID NO:188.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length  
30 protein coding sequence of clone CW823\_3 deposited with the ATCC under accession number 98292;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW823\_3 deposited with the ATCC under accession number 98292;
- 5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:190;
- 10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:190;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:189.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589; the nucleotide sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627; the nucleotide sequence of the full-length protein coding sequence of clone CW823\_3 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CW823\_3 deposited with the
- 25 ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment preferably
- 30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:190, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:190.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
35 NO:189.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

5 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:189, but excluding the poly(A) tail at the 3' end of SEQ ID NO:189; and

10 (ab) the nucleotide sequence of the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

15 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:189, but excluding the poly(A) tail at the 3' end of SEQ ID NO:189; and

(bb) the nucleotide sequence of the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:189 to a nucleotide  
30 sequence corresponding to the 3' end of SEQ ID NO:189, but excluding the poly(A) tail at the 3' end of SEQ ID NO:189. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide  
35 589, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:189

from nucleotide 401 to nucleotide 589. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:190;
  - 10 (b) a fragment of the amino acid sequence of SEQ ID NO:190, the fragment comprising eight contiguous amino acids of SEQ ID NO:190; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;
- the protein being substantially free from other mammalian proteins. Preferably such protein
- 15 comprises the amino acid sequence of SEQ ID NO:190. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:190, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity,
  - 20 the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:190.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length
- 30 protein coding sequence of clone DF989\_3 deposited with the ATCC under accession number 98292;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DF989\_3 deposited with the ATCC under accession number 98292;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:192;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:192;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:191.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868; the nucleotide sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868; the nucleotide sequence of the full-length protein coding sequence of clone DF989\_3 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone DF989\_3 deposited with the  
25 ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:192 from amino acid 75 to amino acid 107. In further preferred  
30 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:192, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising the  
35 amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:192.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:191 and SEQ ID NO:193.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:191;
    - 10 (ab) SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193; and
    - (ac) the nucleotide sequence of the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions
  - 15 at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in
  - 20 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:191;
    - (bb) SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193; and
    - 25 (bc) the nucleotide sequence of the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - 30 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:191 and SEQ ID NO:193, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:191 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:193, but excluding

35 the poly(A) tail at the 3' end of SEQ ID NO:193. Also preferably the polynucleotide isolated

according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:191 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:191. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:192;
- (b) the amino acid sequence of SEQ ID NO:192 from amino acid 75 to amino acid 107;
- (c) a fragment of the amino acid sequence of SEQ ID NO:192, the fragment comprising eight contiguous amino acids of SEQ ID NO:192; and
- (d) the amino acid sequence encoded by the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:192 or the amino acid sequence of SEQ ID NO:192 from amino acid 75 to amino acid 107. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:192, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:192.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:194;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DL162\_1 deposited with the ATCC under accession number 98292;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DL162\_1 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:195;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:195;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:194.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787; the nucleotide sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787; the nucleotide sequence of the full-length protein coding sequence of clone DL162\_1 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone DL162\_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide

30 encodes the full-length or a mature protein encoded by the cDNA insert of clone DL162\_1

35



deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:195 from amino acid 38 to amino acid 170. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:195, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment comprising the amino acid sequence from amino acid 84 to amino acid 93 of SEQ ID NO:195.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:194.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:194, but excluding the poly(A) tail at the 3' end of SEQ ID NO:194; and
    - 20 (ab) the nucleotide sequence of the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
  - 25 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 30 (ba) SEQ ID NO:194, but excluding the poly(A) tail at the 3' end of SEQ ID NO:194; and
    - (bb) the nucleotide sequence of the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions
    - 35 at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:194, and extending contiguously  
5 from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:194 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:194, but excluding the poly(A) tail at the 3' end of SEQ ID NO:194. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787, and extending contiguously from a nucleotide sequence  
10 corresponding to the 5' end of said sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787, and extending contiguously from a nucleotide  
15 sequence corresponding to the 5' end of said sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:195;
- (b) the amino acid sequence of SEQ ID NO:195 from amino acid 38 to amino acid 170;
- (c) a fragment of the amino acid sequence of SEQ ID NO:195, the fragment comprising eight contiguous amino acids of SEQ ID NO:195; and
- 25 (d) the amino acid sequence encoded by the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:195 or the amino acid sequence of SEQ ID NO:195 from amino acid 38 to amino acid 170. In further preferred embodiments, the present  
30 invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:195, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment comprising the amino acid sequence from amino acid 84 to amino acid 93 of SEQ  
35 ID NO:195.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196  
5 from nucleotide 121 to nucleotide 3345;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196  
from nucleotide 160 to nucleotide 3345;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196  
from nucleotide 2592 to nucleotide 3318;
- 10 (e) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone DL162\_2 deposited with the ATCC under accession  
number 98292;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone DL162\_2 deposited with the ATCC under accession number 98292;
- 15 (g) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone DL162\_2 deposited with the ATCC under accession number  
98292;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone DL162\_2 deposited with the ATCC under accession number 98292;
- 20 (i) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:197;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:197 having biological activity, the fragment comprising  
eight contiguous amino acids of SEQ ID NO:197;
- 25 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)  
above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i)  
or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the  
length of SEQ ID NO:196.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:196  
35 from nucleotide 121 to nucleotide 3345; the nucleotide sequence of SEQ ID NO:196 from

nucleotide 160 to nucleotide 3345; the nucleotide sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318; the nucleotide sequence of the full-length protein coding sequence of clone DL162\_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone DL162\_2 deposited with the ATCC under  
5 accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DL162\_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:197 from amino acid 860 to amino acid 1066. In further preferred embodiments, the present  
10 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:197, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment comprising the amino acid sequence from  
15 amino acid 532 to amino acid 541 of SEQ ID NO:197.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:196.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (aa) SEQ ID NO:196, but excluding the poly(A) tail at the 3' end of SEQ ID NO:196; and
    - (ab) the nucleotide sequence of the cDNA insert of clone DL162\_2 deposited with the ATCC under accession number 98292;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- 35 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:196, but excluding the poly(A) tail at the 3' end of SEQ ID NO:196; and

(bb) the nucleotide sequence of the cDNA insert of clone DL162\_2 deposited with the ATCC under accession number 98292;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:196 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:196, but excluding the poly(A) tail at the 3' end of SEQ ID NO:196. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:196

15 from nucleotide 121 to nucleotide 3345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:196 from nucleotide 121 to nucleotide 3345, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:196 from nucleotide 121 to nucleotide 3345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of

20 SEQ ID NO:196 from nucleotide 160 to nucleotide 3345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:196 from nucleotide 160 to nucleotide 3345, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:196 from nucleotide 160 to nucleotide 3345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

25 corresponding to the cDNA sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:197;

(b) the amino acid sequence of SEQ ID NO:197 from amino acid 860 to amino acid 1066;

- (c) a fragment of the amino acid sequence of SEQ ID NO:197, the fragment comprising eight contiguous amino acids of SEQ ID NO:197; and
- (d) the amino acid sequence encoded by the cDNA insert of clone DL162\_2 deposited with the ATCC under accession number 98292;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:197 or the amino acid sequence of SEQ ID NO:197 from amino acid 860 to amino acid 1066. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment preferably comprising eight (more preferably
- 10 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:197, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment comprising the amino acid sequence from amino acid 532 to amino acid 541 of SEQ ID NO:197.

In one embodiment, the present invention provides a composition comprising an isolated

15 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198
- 20 from nucleotide 2130 to nucleotide 2600;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone EC172\_1 deposited with the ATCC under accession
- 25 number 98292;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone EC172\_1 deposited with the ATCC under accession number
- 30 98292;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:199;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:199;

5 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

10 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:198.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600; the nucleotide sequence of SEQ ID NO:198 from  
15 nucleotide 2130 to nucleotide 2600; the nucleotide sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506; the nucleotide sequence of the full-length protein coding sequence of clone EC172\_1 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone EC172\_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a  
20 mature protein encoded by the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:199 from amino acid 1 to amino acid 130. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
25 ID NO:199 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:199, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment comprising the amino acid sequence from amino acid 409 to amino acid 418 of SEQ ID NO:199.

30 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:198.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198; and

(ab) the nucleotide sequence of the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198; and

(bb) the nucleotide sequence of the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;

20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

25 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:198 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198

30 from nucleotide 117 to nucleotide 2600, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of

35 SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600, and extending contiguously from a



nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506.

In other embodiments, the present invention provides a composition comprising a protein,  
10 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:199;
- (b) the amino acid sequence of SEQ ID NO:199 from amino acid 1 to amino acid 130;
- (c) a fragment of the amino acid sequence of SEQ ID NO:199, the fragment  
15 comprising eight contiguous amino acids of SEQ ID NO:199; and
- (d) the amino acid sequence encoded by the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:199 or the amino acid sequence of SEQ ID  
20 NO:199 from amino acid 1 to amino acid 130. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:199, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity,  
25 the fragment comprising the amino acid sequence from amino acid 409 to amino acid 418 of SEQ ID NO:199.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the  
30 present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- 35 (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

- 5       Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

10                               BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

DETAILED DESCRIPTION

15   ISOLATED PROTEINS AND POLYNUCLEOTIDES

- Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be  
20   determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

- 25       As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported  
30   across the membrane of the endoplasmic reticulum.

Clone "AX65\_22"

- A polynucleotide of the present invention has been identified as clone "AX65\_22". AX65\_22 was isolated from a human adult testes cDNA library using methods which are selective  
35   for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding

a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AX65\_22 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AX65\_22 protein").

5 The nucleotide sequence of the 5' portion of AX65\_22 as presently determined is reported in SEQ ID NO:1. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:2. The predicted amino acid sequence of the AX65\_22 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 8 to 20 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted  
10 leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AX65\_22 protein. Additional nucleotide sequence from the 3' portion of AX65\_22, including a poly(A) tail, is reported in SEQ ID NO:3.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
15 AX65\_22 should be approximately 3500 bp.

The nucleotide sequence disclosed herein for AX65\_22 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AX65\_22 demonstrated at least some similarity with sequences identified as T08476 (Eukaryotic expression vector pAPEX-3p) and U46493 (Cloning vector pFlp recombinase  
20 gene, complete cds). The predicted AX65\_22 protein demonstrated at least some homology with sequences identified as J01969 (DNA polymerase [Human adenovirus type 5]), R07640 (Deduced protein sequence of p170-2 comprising T4), and X57205 (fibroblast growth factor receptor [Homo sapiens]). Based upon sequence similarity, AX65\_22 proteins and each similar protein or peptide may share at least  
25 some activity.

#### Clone "BD335\_14"

A polynucleotide of the present invention has been identified as clone "BD335\_14". BD335\_14 was isolated from a human fetal kidney cDNA library using methods which are  
30 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD335\_14 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD335\_14 protein").

The nucleotide sequence of BD335\_14 as presently determined is reported in SEQ ID  
35 NO:4, and includes a poly(A) tail. What applicants presently believe to be the proper reading

frame and the predicted amino acid sequence of the BD335\_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:5.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD335\_14 should be approximately 3000 bp.

- 5       The nucleotide sequence disclosed herein for BD335\_14 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. The predicted BD335\_14 protein demonstrated at least some similarity with sequences identified as U83511 (APXL [Homo sapiens]). Based upon sequence similarity, BD335\_14 proteins and each homologous protein or peptide may share at least some activity. The
- 10   TopPredII computer program predicts three potential transmembrane domains within the BD335\_14 protein sequence, one centered around amino acid 80, another around amino acid 320, and a third around amino acid 700 of SEQ ID NO:5.

Clone "BG241\_1"

- 15       A polynucleotide of the present invention has been identified as clone "BG241\_1". BG241\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG241\_1 is a full-length clone, including the entire coding sequence of
- 20   a secreted protein (also referred to herein as "BG241\_1 protein").

- The nucleotide sequence of the 5' portion of BG241\_1 as presently determined is reported in SEQ ID NO:6. An additional internal nucleotide sequence from BG241\_1 as presently determined is reported in SEQ ID NO:7. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:8.
- 25   Additional nucleotide sequence from the 3' portion of BG241\_1, including a poly(A) tail, is reported in SEQ ID NO:9.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG241\_1 should be approximately 800 bp.

- The nucleotide sequence disclosed herein for BG241\_1 was searched against the GenBank
- 30   and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG241\_1 demonstrated at least some similarity with sequences identified as AI082187 (ox75f01.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE 1662169 3' similar to contains element MSR1 repetitive element; mRNA sequence), W38781 (zb27g08.r1 Soares parathyroid tumor NbHPA Homo sapiens), and Y12781 (Homo sapiens
- 35   mRNA for transducin (beta) like 1 protein). The predicted BG241\_1 protein demonstrated at

least some similarity to sequences identified as Y12781 (transducin (beta) like 1 protein [Homo sapiens]) and other beta-transducin-like proteins (see GenBank accession numbers L28125 and T86738). Based upon sequence similarity, BG241\_1 proteins and each similar protein or peptide may share at least some activity.

5

Clone "BL187\_4"

A polynucleotide of the present invention has been identified as clone "BL187\_4". BL187\_4 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
10 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BL187\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BL187\_4 protein").

The nucleotide sequence of BL187\_4 as presently determined is reported in SEQ ID NO:10, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
15 frame and the predicted amino acid sequence of the BL187\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:11. Amino acids 17 to 29 of SEQ ID NO:11 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal  
20 sequence not be separated from the remainder of the BL187\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BL187\_4 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for BL187\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
25 protocols. BL187\_4 demonstrated at least some similarity with sequences identified as AA476210 (zw35g01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 771312 3', mRNA sequence), AA868505 (ak43b04.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE 1408687 3' similar to SW PLZF\_HUMAN Q05516 ZINC FINGER PROTEIN PLZF; mRNA sequence), AA927876 (om18b09.s1 Soares NFL T GBC S1  
30 Homo sapiens cDNA clone IMAGE:1541369 3', mRNA sequence), AD000671 (Homo sapiens DNA from chromosome 19-cosmid f24109 containing HRX2, genomic sequence), H48938 (EST0010 Homo sapiens cDNA clone HTN-6-15), and Z63958 (H.sapiens CpG DNA, clone 93d10, forward read cpg93d10.f1a). The predicted amino acid sequence disclosed herein for BL187\_4 was searched against the GenPept and GeneSeq amino acid

sequence databases using the BLASTX search protocol. The predicted BL187\_4 protein demonstrated at least some similarity to sequences identified as R95242 (HIC-1 polypeptide), Z19002 (kruppel-like zinc finger protein [Homo sapiens]), and a number of other zinc-finger proteins. Based upon sequence similarity, BL187\_4 proteins and each similar protein or peptide may share at least some activity. Motifs analysis indicates the presence of two zinc-finger (C2H2 type) domains centered around amino acids 375 and 430 of SEQ ID NO:11, respectively. The TopPredII computer program predicts two potential transmembrane domains within the BL187\_4 protein sequence, one centered around amino acid 30 and another around amino acid 260 of SEQ ID NO:11. BL187\_4 protein appears to be a novel secreted or membrane-associated zinc-finger protein.

#### Clone "BL249\_18"

A polynucleotide of the present invention has been identified as clone "BL249\_18". BL249\_18 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BL249\_18 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BL249\_18 protein").

The nucleotide sequence of BL249\_18 as presently determined is reported in SEQ ID NO:12, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BL249\_18 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:13. Amino acids 32 to 44 of SEQ ID NO:13 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 45. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BL249\_18 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BL249\_18 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for BL249\_18 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BL249\_18 demonstrated at least some similarity with sequences identified as AA034864 (mi53f01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 467257 5'), AA115100 (zl02h12.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 491207 3'), AA219365 (zr04c06.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 650506 5'), AA399095 (zt59b06.r1 Soares

testis NHT Homo sapiens cDNA clone 726611 5'), R82633 (yj20a05.s1 Homo sapiens cDNA clone 149264 3'), and T22047 (Human gene signature HUMGS03590). The predicted amino acid sequence disclosed herein for BL249\_18 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted

5 BL249\_18 protein demonstrated at least some similarity to sequences identified as AC003673 (unknown protein (AAC09020.1) [Arabidopsis thaliana]) and Z98598 (hypothetical protein [Schizosaccharomyces pombe]). Based upon sequence similarity, BL249\_18 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the BL249\_18 protein sequence, one

10 centered around amino acid 45 and another around amino acid 680 of SEQ ID NO:13.

#### Clone "BO71\_1"

A polynucleotide of the present invention has been identified as clone "BO71\_1". BO71\_1 was isolated from a human adult retina cDNA library using methods which are selective

15 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO71\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO71\_1 protein").

The nucleotide sequence of the 5' portion of BO71\_1 as presently determined is reported

20 in SEQ ID NO:14. An additional internal nucleotide sequence from BO71\_1 as presently determined is reported in SEQ ID NO:15. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:16. Additional nucleotide sequence from the 3' portion of BO71\_1, including a poly(A) tail, is reported in SEQ ID NO:17.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO71\_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for BO71\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO71\_1 demonstrated at least some similarity with sequences identified as X86809

30 (H.sapiens mRNA for major astrocytic phosphoprotein PEA-15). The predicted amino acid sequence disclosed herein for BO71\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO71\_1 protein demonstrated at least some similarity to sequences identified as U06144 (cellular disintegrin-related protein [Mus musculus]). Based upon sequence similarity, BO71\_1

35 proteins and each similar protein or peptide may share at least some activity.

Clone "BO365\_2"

A polynucleotide of the present invention has been identified as clone "BO365\_2". BO365\_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO365\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO365\_2 protein").

The nucleotide sequence of BO365\_2 as presently determined is reported in SEQ ID NO:18, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
10 frame and the predicted amino acid sequence of the BO365\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:19.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO365\_2 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for BO365\_2 was searched against the GenBank  
15 and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO365\_2 demonstrated at least some similarity with sequences identified as D63876 (Human mRNA for KIAA0154 gene, partial cds) and Z83844 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16; HTGS phase 1). The predicted amino acid sequence disclosed herein for BO365\_2 was searched against the GenPept and  
20 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO365\_2 protein demonstrated at least some similarity to sequences identified as D10250 (alpha-fetoprotein enhancer binding protein [Homo sapiens]), D63876 (KIAA0154 gene product is related to mouse gamma adaptin [Homo sapiens]), and R23962 (AFP-1). Based upon sequence similarity, BO365\_2 proteins and each similar protein or peptide may share at least  
25 some activity. The TopPredII computer program predicts three potential transmembrane domains within the BO365\_2 protein sequence, centered around amino acids 70, 140, and 180 of SEQ ID NO:19, respectively.

Clone "BV51\_1"

A polynucleotide of the present invention has been identified as clone "BV51\_1". BV51\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
30 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV51\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV51\_1 protein").  
35



The nucleotide sequence of the 5' portion of BV51\_1 as presently determined is reported in SEQ ID NO:20. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:21. The predicted amino acid sequence of the BV51\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:21. Additional  
5 nucleotide sequence from the 3' portion of BV51\_1, including a poly(A) tail, is reported in SEQ ID NO:22.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV51\_1 should be approximately 970 bp.

The nucleotide sequence disclosed herein for BV51\_1 was searched against the GenBank  
10 and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV51\_1 demonstrated at least some similarity with sequences identified as AB012130 (Homo sapiens SBC2 mRNA for sodium bicarbonate cotransporter2, complete cds) and U46493 (Cloning vector pFlp recombinase gene, complete cds). The predicted amino acid  
15 sequence disclosed herein for BV51\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BV51\_1 protein demonstrated at least some similarity to sequences identified as AB01213 (sodium bicarbonate cotransporter2 [Homo sapiens]). Based upon sequence similarity, BV51\_1 proteins and each similar protein or peptide may share at least some activity.

20 Clone "BV140\_3"

A polynucleotide of the present invention has been identified as clone "BV140\_3". BV140\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence  
25 of the encoded protein. BV140\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV140\_3 protein").

The nucleotide sequence of the 5' portion of BV140\_3 as presently determined is reported in SEQ ID NO:23. An additional internal nucleotide sequence from BV140\_3 as presently determined is reported in SEQ ID NO:24. What applicants believe is the proper reading frame  
30 and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:25. Additional nucleotide sequence from the 3' portion of BV140\_3, including a poly(A) tail, is reported in SEQ ID NO:26.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV140\_3 should be approximately 3500 bp.

The nucleotide sequence disclosed herein for BV140\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV140\_3 demonstrated at least some similarity with sequences identified as H72799 (yu07d10.r1 Homo sapiens cDNA clone 233107 5') and T94057 (ye33g08.r1 Homo sapiens cDNA clone 119582 5'). Based upon sequence similarity, BV140\_3 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BV141\_2"

A polynucleotide of the present invention has been identified as clone "BV141\_2". BV141\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV141\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV141\_2 protein").

The nucleotide sequence of BV141\_2 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV141\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV141\_2 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for BV141\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV141\_2 demonstrated at least some similarity with sequences identified as L26860 (Mus musculus (C6e) heavy chain immunoglobulin variable region gene). Based upon sequence similarity, BV141\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the BV141\_2 protein sequence, one centered around amino acid 34 and another around amino acid 65 of SEQ ID NO:28. The nucleotide sequence of BV141\_2 indicates that it may contain one or more of the following repetitive element(s): L1 repeat.

#### Clone "CC194\_4"

A polynucleotide of the present invention has been identified as clone "CC194\_4". CC194\_4 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. CC194\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC194\_4 protein").

The nucleotide sequence of the 5' portion of CC194\_4 as presently determined is reported in SEQ ID NO:29. What applicants presently believe is the proper reading frame for the coding  
5 region is indicated in SEQ ID NO:30. The predicted amino acid sequence of the CC194\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 88 to 100 of SEQ ID NO:30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 101. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted  
10 leader/signal sequence not be separated from the remainder of the CC194\_4 protein. Additional nucleotide sequence from the 3' portion of CC194\_4, including a poly(A) tail, is reported in SEQ ID NO:31.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CC194\_4 should be approximately 3300 bp.

15 The nucleotide sequence disclosed herein for CC194\_4 was searched against the GenBank and GeneSeq nucleotide sequence databascs using BLASTN/BLASTX and FASTA search protocols. CC194\_4 demonstrated at least some similarity with sequences identified as AA722214 (zh20f10.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone 412651 3', mRNA sequence), H11476 (ym10h08.s1 Homo sapiens cDNA clone 47781 3'), H11581  
20 (ym10h08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:47781 5' similar to SP:C36E8.3 CE00911; mRNA sequence), H23044 (ym51d07.r1 Homo sapiens cDNA clone 52058 5' similar to SP:C36E8.3 CE00911), N93789 (zb64g05.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 308408 3'), and W54544 (mc99a01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus). The predicted amino acid sequence disclosed  
25 herein for CC194\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CC194\_4 protein demonstrated at least some similarity to sequences identified as M38561 (CAD [Homo sapiens]). Based upon sequence similarity, CC194\_4 proteins and each similar protein or peptide may share at least some activity.

30

#### Clone "DA136\_11"

A polynucleotide of the present invention has been identified as clone "DA136\_11".  
35 DA136\_11 was isolated from a human adult placenta cDNA library using methods which are

selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DA136\_11 includes at least a portion of the coding sequence of a secreted protein (also referred to herein as "DA136\_11 protein").

5       The nucleotide sequence of DA136\_11 as presently determined is reported in SEQ ID NO:32, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the DA136\_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:33.

10       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DA136\_11 should be approximately 3800 bp.

15       The nucleotide sequence disclosed herein for DA136\_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. DA136\_11 demonstrated at least some similarity with sequences identified as AA523414 (ng30a07.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone 936276), H89334 (yw25h09.r1 Homo sapiens cDNA clone 253313 5'), R59925 (yh11b12.s1 Homo sapiens cDNA clone 42891 3), T66165 (Human interleukin-12 receptor alpha chain NR4 DNA), Y09328 (H.sapiens mRNA for IL13 receptor alpha-1 chain), and Y10659 (H.sapiens IL-13Ra mRNA). The predicted amino acid sequence disclosed herein for DA136\_11 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX  
20       search protocol. The predicted DA136\_11 protein demonstrated at least some similarity to sequences identified as L08960 (cell adhesion molecule [Gallus gallus]), M34083 (lactogen receptor precursor [Rattus norvegicus]), M59941 (GM-CSF receptor beta chain [Homo sapiens]), W09822 (Human interleukin-12 receptor alpha chain NR4), X61178 (interleukin-5 receptor type 3 [Homo sapiens]), and Y10659 (IL-13Ra [Homo sapiens]).  
25       Based upon sequence similarity, DA136\_11 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the DA136\_11 protein sequence, centered around amino acid 215 of SEQ ID NO:33.

30       Clone "AR415\_4"

A polynucleotide of the present invention has been identified as clone "AR415\_4". AR415\_4 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. AR415\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AR415\_4 protein").

The nucleotide sequence of AR415\_4 as presently determined is reported in SEQ ID NO:34, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
 5 frame and the predicted amino acid sequence of the AR415\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:35. Amino acids 14 to 26 of SEQ ID NO:35 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal  
 10 sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AR415\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AR415\_4 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for AR415\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
 15 protocols. AR415\_4 demonstrated at least some similarity with sequences identified as AA100799 (zm26d01.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526753 3'), AA100852 (zm26d01.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526753 5' similar to SW CO02\_HUMAN P19075 TUMOR-ASSOCIATED ANTIGEN CO-029), AA146605 (zo35c09.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 588880 5' similar to  
 20 SW:CO02\_HUMAN P19075 TUMOR-ASSOCIATED ANTIGEN CO-029), AA224847 (nc33c12.s1 NCI CGAP Pr2 Homo sapiens cDNA clone 4079 similar to SW:CO02\_HUMAN P19075 TUMOR-ASSOCIATED ANTIGEN CO-029), AA225191 (nc21h08.s1 NCI CGAP Pr1 Homo sapiens cDNA clone 2968), AA593864 (nn19f08.s1 NCI CGAP Co12 Homo sapiens cDNA clone IMAGE:1084359), D26483 (Mouse mRNA for PE31/TALLA), M33680 (Human  
 25 26-kDa cell surface protein TAPA-1 mRNA, complete cds), T14726 (Human CD53 antigen cDNA), and T23814 (Human gene signature HUMGS05723). The predicted amino acid sequence disclosed herein for AR415\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AR415\_4 protein demonstrated at least some sequence similarity with sequences identified as D29808 (TALLA-1  
 30 [Homo sapiens]), M35252 (tumor-associated antigen [Homo sapiens]), and R22360 (CO-029 tumour associated antigen protein). Based upon sequence similarity, AR415\_4 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the AR415\_4 protein sequence centered around amino acid 100 of SEQ ID NO:35.

Clone "AS63\_29"

A polynucleotide of the present invention has been identified as clone "AS63\_29". AS63\_29 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AS63\_29 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AS63\_29 protein").

The nucleotide sequence of the 5' portion of AS63\_29 as presently determined is reported in SEQ ID NO:36. What applicants presently believe is the proper reading frame for the coding  
10 region is indicated in SEQ ID NO:37. The predicted amino acid sequence of the AS63\_29 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:37. Amino acids 28 to 40 of SEQ ID NO:37 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted  
15 leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AS63\_29 protein. Additional nucleotide sequence from the 3' portion of AS63\_29, including a poly(A) tail, is reported in SEQ ID NO:38.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AS63\_29 should be approximately 1700 bp.

20 The nucleotide sequence disclosed herein for AS63\_29 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AS63\_29 demonstrated at least some similarity with sequences identified as L26877 (Mus musculus (B20c) heavy chain immunoglobulin variable region gene), T09146 (EST07039 Homo sapiens cDNA clone HIBBP68 5' end), T23466 (seq3050 Homo sapiens cDNA clone  
25 Hy18-Ch13-Charon40-cDNA-100 3'), and W55739 (ma35f05.r1 Life Tech mouse brain Mus musculus cDNA clone 312705 5'). The predicted amino acid sequence disclosed herein for AS63\_29 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AS63\_29 protein demonstrated at least some  
30 sequence similarity with sequences identified as R04032 (Full length T4 encoded by plasmid pBG381). Based upon sequence similarity, AS63\_29 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the AS63\_29 protein sequence, near the amino terminus.

Clone "AY304\_14"

A polynucleotide of the present invention has been identified as clone "AY304\_14". AY304\_14 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AY304\_14 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AY304\_14 protein").

The nucleotide sequence of AY304\_14 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AY304\_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AY304\_14 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for AY304\_14 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AY304\_14 demonstrated at least some similarity with sequences identified as AA127688 (zk92f05.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490305 3'), AA179609 (zp49g11.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 612836 5'), AA276253 (vc40f05.r1 Barstead MPLRB1 Mus musculus cDNA clone 777057 5'), H15545 (ym27d04.s1 Homo sapiens cDNA clone 49495 3' similar to contains PTR5 repetitive element), L08441 (Human autonomously replicating sequence (ARS) mRNA), N34949 (yy49h09.s1 Homo sapiens cDNA clone 276929 3'), R48594 (yj65d07.s1 Homo sapiens cDNA clone 153613 3'), T21160 (Human gene signature HUMGS02466), U43284 (Cloning vector phGFP-S65T, complete sequence, green fluorescent protein (gfp) gene, complete cds), and Z45151 (H. sapiens partial cDNA sequence; clone c-2hh04). The predicted amino acid sequence disclosed herein for AY304\_14 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AY304\_14 protein demonstrated at least some sequence similarity with sequences identified as D86984 (similar to yeast adenylate cyclase (S56776) [Homo sapiens]), J01415 (cytochrome oxidase subunit 3 [Homo sapiens]), V00662 (cytochrome oxidase III [Homo sapiens]), and X68948 (envelope glycoprotein [Spleen focus-forming virus]). Based upon sequence similarity, AY304\_14 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the AY304\_14 protein sequence, one centered around amino acid 81 and another around amino acid 120 of SEQ ID NO:40.

35           Clone "BG160\_1"

A polynucleotide of the present invention has been identified as clone "BG160\_1". BG160\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG160\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG160\_1 protein").

The nucleotide sequence of BG160\_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG160\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 588 to 600 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 601. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BG160\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG160\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for BG160\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG160\_1 demonstrated at least some similarity with sequences identified as A60021 (tropomyosin-related protein, neuronal - rat ;contains element MER27 repetitive element), AA081525 (zn20e02.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547994 5'), AA092565 (ll5773.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'), D56138 (Human fetal brain cDNA 5'-end GEN-416H11), D61090 (Human fetal brain cDNA 5'-end GEN-155A07), D61184 (Human fetal brain cDNA 5'-end GEN-165A01), L10335 (Homo sapiens neuro-endocrine-specific protein C (NSP) mRNA, complete cds), N21304 (yx53f07.s1 Homo sapiens cDNA clone 265477 3' similar to SP:A60021 A60021 TROPOMYOSIN-RELATED PROTEIN, NEURONAL), and W95814 (ze07f11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358317 5' similar to PIR:A60021). The predicted amino acid sequence disclosed herein for BG160\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG160\_1 protein demonstrated at least some sequence similarity with sequences identified as L10334 (neuroendocrine-specific protein B [Homo sapiens]), L10335 (neuroendocrine-specific protein C [Homo sapiens]). Based upon sequence similarity, BG160\_1 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer



program predicts three potential transmembrane domains within the BG160\_1 protein sequence, centered around amino acids 84, 484, and 595 of SEQ ID NO:42, respectively.

BG160\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 110 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "BO432\_4"

A polynucleotide of the present invention has been identified as clone "BO432\_4". BO432\_4 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO432\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO432\_4 protein").

The nucleotide sequence of the 5' portion of BO432\_4 as presently determined is reported in SEQ ID NO:43. An additional internal nucleotide sequence from BO432\_4 as presently determined is reported in SEQ ID NO:44. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:45. Additional nucleotide sequence from the 3' portion of BO432\_4, including a poly(A) tail, is reported in SEQ ID NO:46.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO432\_4 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for BO432\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO432\_4 demonstrated at least some similarity with sequences identified as AA283626 (zt15e09.s1 Soares NbHTGBC Homo sapiens cDNA clone 713224 3'), AA406486 (zv12g02.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753458 5' similar to WP F35G2.2 CE05809 E.COLI YCAC LIKE), AA570446 (nk62c12.s1 NCI CGAP\_Sch1 Homo sapiens cDNA clone IMAGE:1018102), N55855 (J3389F Homo sapiens cDNA clone J3389 5'), Q10613 (Rianodin receptor gene), T62691 (yc70d10.r1 Homo sapiens cDNA clone 86035 5'), and W90766 (zh79h04.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 418327 3'). The predicted amino acid sequence disclosed herein for BO432\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO432\_4 protein demonstrated at least some sequence similarity with sequences identified as Z69637 (F35G2.2 [Caenorhabditis elegans]). Based upon sequence similarity, BO432\_4 proteins and each homologous protein or peptide may share at least some activity. The TopPredII

computer program predicts a potential transmembrane domain at the amino terminus of the BO432\_4 protein sequence. The BO432\_4 protein may also contain the bacterial lysR family signature, a motif found in bacterial transcriptional regulators and which is possibly indicative of a helix-turn-helix structure.

5

Clone "BO538\_2"

A polynucleotide of the present invention has been identified as clone "BO538\_2". BO538\_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
10 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO538\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO538\_2 protein").

The nucleotide sequence of the 5' portion of BO538\_2 as presently determined is reported in SEQ ID NO:47. What applicants presently believe is the proper reading frame for the coding  
15 region is indicated in SEQ ID NO:48. The predicted amino acid sequence of the BO538\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Additional nucleotide sequence from the 3' portion of BO538\_2, including a poly(A) tail, is reported in SEQ ID NO:49.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 BO538\_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BO538\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO538\_2 demonstrated at least some similarity with sequences identified as AA503100 (ne44h01.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone 900241), R44035  
25 (yg21g09.s1 Homo sapiens cDNA clone 33167 3'), T21630 (Human gene signature HUMGS03066), and W64854 (me06d12.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 386711 5' similar to PIR S40989 S40989 hypothetical protein F55H2.6 - Caenorhabditis elegans). The predicted amino acid sequence disclosed herein for BO538\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX  
30 search protocol. The predicted BO538\_2 protein demonstrated at least some sequence similarity with sequences identified as M60525 (nerve growth factor inducible protein [Rattus norvegicus]), R28916 (Type III procollagen), and Z27080 (F55H2.6 [Caenorhabditis elegans]). Based upon sequence similarity, BO538\_2 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains  
35 within the BO538\_2 protein sequence.

Clone "BR595\_4"

A polynucleotide of the present invention has been identified as clone "BR595\_4". BR595\_4 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BR595\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BR595\_4 protein").

The nucleotide sequence of the 5' portion of BR595\_4 as presently determined is reported in SEQ ID NO:50. What applicants presently believe is the proper reading frame for the coding  
10 region is indicated in SEQ ID NO:51. The predicted amino acid sequence of the BR595\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:51. Additional nucleotide sequence from the 3' portion of BR595\_4, including a poly(A) tail, is reported in SEQ ID NO:52.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
15 BR595\_4 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BR595\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BR595\_4 demonstrated at least some similarity with sequences identified as AA443742 (zw95b02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784683 3'),  
20 AA600820 (np45b08.s1 NCI\_CGAP\_Br1.1 Homo sapiens cDNA clone IMAGE:1129239), T19410 (Human gene signature HUMGS00435), W87465 (zh67c04.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417126 3'), and Z33587 (H. sapiens partial cDNA sequence; clone HEA89P; single read). Based upon sequence similarity, BR595\_4 proteins and each homologous protein or peptide may share at least some activity.

25

Clone "CI490\_2"

A polynucleotide of the present invention has been identified as clone "CI490\_2". CI490\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
30 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CI490\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CI490\_2 protein").

The nucleotide sequence of CI490\_2 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
35 frame and the predicted amino acid sequence of the CI490\_2 protein corresponding to the

foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 64 to 76 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 77. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CI490\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CI490\_2 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for CI490\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CI490\_2 demonstrated at least some similarity with sequences identified as H30751 (yo79a04.r1 Homo sapiens cDNA clone 184110 5'), H49766 (yo24f01.r1 Homo sapiens cDNA clone 178873 5' similar to SP:S19586 N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN), H51158 (yo32d04.r1 Homo sapiens cDNA clone 179623 5'), R85211 (yo41d11.s1 Homo sapiens cDNA clone 180501 3' similar to SP S19586 N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN), S19586 (N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN), S61973 (NMDA receptor glutamate-binding subunit [rat, mRNA]), T01031 (Human leucine zipper protein-kinase cDNA sequence), and W56893 (zc01g05.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321080 5' similar to PIR S19586 S19586 N-methyl-D-aspartate receptor glutamate-binding chain - rat). The predicted amino acid sequence disclosed herein for CI490\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CI490\_2 protein demonstrated at least some sequence similarity with sequences identified as S61973 (NMDA receptor glutamate-binding subunit [Rattus sp.]) and U08020 (collagen pro-alpha-1 type I chain [Mus musculus]). Based upon sequence similarity, CI490\_2 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the CI490\_2 protein sequence, with the most amino-terminal transmembrane domain centered around amino acid 77 of SEQ ID NO:54.

### 30 Clone "CI522\_1"

A polynucleotide of the present invention has been identified as clone "CI522\_1". CI522\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. CI522\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CI522\_1 protein").

The nucleotide sequence of the 5' portion of CI522\_1 as presently determined is reported in SEQ ID NO:55. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:56. The predicted amino acid sequence of the CI522\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 7 to 19 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CI522\_1 protein. Additional nucleotide sequence from the 3' portion of CI522\_1, including a poly(A) tail, is reported in SEQ ID NO:57.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CI522\_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for CI522\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CI522\_1 demonstrated at least some similarity with sequences identified as AA028557 (mil18g05.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 463928 5'), H32238 (EST107136 Rattus sp. cDNA 5' end), T33525 (EST58140 Homo sapiens cDNA 5' end similar to None), U66468 (Human cell growth regulator CGR11 mRNA, complete cds), and X00525 (Mouse 28S ribosomal RNA). The predicted amino acid sequence disclosed herein for CI522\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CI522\_1 protein demonstrated at least some sequence similarity with sequences identified as U66468 (cell growth regulator CGR11 [Homo sapiens]). Based upon sequence similarity, CI522\_1 proteins and each homologous protein or peptide may share at least some activity.

#### Clone "CN238\_1"

A polynucleotide of the present invention has been identified as clone "CN238\_1". CN238\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CN238\_1 includes at least a portion of the coding sequence of a secreted protein (also referred to herein as "CN238\_1 protein").

The nucleotide sequence of CN238\_1 as presently determined is reported in SEQ ID NO:58, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CN238\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:59.

- 5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CN238\_1 should be approximately 2190 bp.

          The nucleotide sequence disclosed herein for CN238\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CN238\_1 demonstrated at least some similarity with sequences identified as  
10   AA044097 (zk51b02.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486315 5'),  
AA044287 (zk51b02.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486315 3'),  
AA045440 (zk67c03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 487876 3'),  
AA143007 (zl48f01.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505177 5'),  
D51196 (Human fetal brain cDNA 3'-end GEN-016G05), D60310 (Human fetal brain cDNA  
15   3'-end GEN-098A09), N69344 (yz43e04.s1 Homo sapiens cDNA clone 285822 3' similar to  
gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN)), W22250 (64B8 Human retina cDNA  
Tsp509I-cleaved sublibrary Homo), and X01703 (Human gene for alpha-tubulin (b alpha 1)). The  
predicted amino acid sequence disclosed herein for CN238\_1 was searched against the GenPept  
and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted  
20   CN238\_1 protein demonstrated at least some sequence similarity with sequences identified as  
K00557 (alpha-tubulin [Homo sapiens]) and U51583 (zinc finger homeodomain enhancer-binding  
protein-1 [Rattus norvegicus]). Based upon sequence similarity, CN238\_1 proteins and each  
homologous protein or peptide may share at least some activity.

25           Clone "CO390\_1"

          A polynucleotide of the present invention has been identified as clone "CO390\_1".  
CO390\_1 was isolated from a human adult brain cDNA library using methods which are selective  
for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence  
30   of the encoded protein. CO390\_1 is a full-length clone, including the entire coding sequence of  
a secreted protein (also referred to herein as "CO390\_1 protein").

          The nucleotide sequence of CO390\_1 as presently determined is reported in SEQ ID  
NO:60, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
frame and the predicted amino acid sequence of the CO390\_1 protein corresponding to the  
35   foregoing nucleotide sequence is reported in SEQ ID NO:61.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO390\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for CO390\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO390\_1 demonstrated at least some similarity with sequences identified as H84353 (y85a11.r1 Homo sapiens cDNA clone 249500 5'), L35532 (Pan troglodytes Alu repeat region), N80616 (Genomic clone encoding SAP(Phe)), R53922 (y03h10.s1 Homo sapiens cDNA clone 138211 3' similar to contains Alu repetitive element; contains TAR1 repetitive element), X75335 (H.sapiens Alu insertion in COL3A1 gene), X95882 (R.norvegicus mRNA for ATP ligand gated ion channel), and Y09561 (H.sapiens mRNA for P2X7 receptor). The predicted amino acid sequence disclosed herein for CO390\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CO390\_1 protein demonstrated at least some sequence similarity with sequences identified as U45448 (P2x1 receptor [Homo sapiens]), W04216 (Rat superior cervical ganglion p2x receptor), X83688 (ATP receptor [Homo sapiens]), X95882 (P2X7 gene product [Rattus norvegicus]), and Y09561 (ATP receptor [Homo sapiens]). Based upon sequence similarity, CO390\_1 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the CO390\_1 protein sequence, centered around amino acid 249 of SEQ ID NO:61. The nucleotide sequence of CO390\_1 may contain an Alu repetitive element.

CO390\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 75 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

25

#### Clone "AJ20\_2"

A polynucleotide of the present invention has been identified as clone "AJ20\_2". AJ20\_2 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AJ20\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AJ20\_2 protein").

The nucleotide sequence of the 5' portion of AJ20\_2 as presently determined is reported in SEQ ID NO:62. What applicants presently believe is the proper reading frame for the coding

35

region is indicated in SEQ ID NO:63. The predicted amino acid sequence of the AJ20\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:63. Amino acids 8 to 20 of SEQ ID NO:63 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AJ20\_2 protein. Additional nucleotide sequence from the 3' portion of AJ20\_2, including a poly(A) tail, is reported in SEQ ID NO:64.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AJ20\_2 should be approximately 850 bp.

The nucleotide sequence disclosed herein for AJ20\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "AR440\_1"

A polynucleotide of the present invention has been identified as clone "AR440\_1". AR440\_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AR440\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AR440\_1 protein").

The partial nucleotide sequence of AR440\_1, including its 3' end and a poly(A) tail, as presently determined is reported in SEQ ID NO:66. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:67. The predicted amino acid sequence of the AR440\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:67. Additional nucleotide sequence from the 5' portion of AR440\_1 is reported in SEQ ID NO:65.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AR440\_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for AR440\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The nucleotide sequence of AR440\_1 indicates that it may contain an Alu repetitive element.

Clone "AS164\_1"



A polynucleotide of the present invention has been identified as clone "AS164\_1". AS164\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AS164\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AS164\_1 protein").

The nucleotide sequence of AS164\_1 as presently determined is reported in SEQ ID NO:68, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AS164\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:69.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AS164\_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for AS164\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AS164\_1 demonstrated at least some similarity with sequences identified as H24668 (yl40h10.r1 Homo sapiens cDNA clone 160771 5'), N29757 (yw90h10.s1 Homo sapiens cDNA clone 259555 3'), T62184 (yb96d08.r1 Homo sapiens cDNA clone 79023 5'), Z69706 (Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin H), and Z69890 (Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island). The predicted amino acid sequence disclosed herein for AS164\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AS164\_1 protein demonstrated at least some similarity to sequences identified as A20359\_1 (ryanodine receptor gene product [Homo sapiens]) and U78866 (putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana]). Based upon sequence similarity, AS164\_1 proteins and each similar protein or peptide may share at least some activity. The predicted AS164\_1 protein sequence also contains repeated Asp-Arg RNA-binding motifs.

#### 30      Clone "AX8\_1"

A polynucleotide of the present invention has been identified as clone "AX8\_1". AX8\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. AX8\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AX8\_1 protein").

The nucleotide sequence of AX8\_1 as presently determined is reported in SEQ ID NO:70, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AX8\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:71. Amino acids 106 to 118 of SEQ ID NO:71 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 119. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AX8\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AX8\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for AX8\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The TopPredII computer program predicts three potential transmembrane domains within the AX8\_1 protein sequence, centered around amino acids 111, 144, and 182 of SEQ ID NO:71, respectively.

AX8\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 35 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "BD176\_3"

A polynucleotide of the present invention has been identified as clone "BD176\_3". BD176\_3 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD176\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD176\_3 protein").

The nucleotide sequence of the 5' portion of BD176\_3 as presently determined is reported in SEQ ID NO:72. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:73. The predicted amino acid sequence of the BD176\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:73. Amino acids 2 to 14 of SEQ ID NO:73 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted

leader/signal sequence not be separated from the remainder of the BD176\_3 protein. Additional nucleotide sequence from the 3' portion of BD176\_3, including a poly(A) tail, is reported in SEQ ID NO:74.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD176\_3 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for BD176\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BD176\_3 demonstrated at least some similarity with sequences identified as AA029679 (ze94g10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366690 5'),  
10 D45913 (Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds), R55610 (yg88h08.r1 Homo sapiens cDNA clone 40606 5'), and T07640 (EST05530 Homo sapiens cDNA clone HFBEM16). The predicted amino acid sequence disclosed herein for BD176\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BD176\_3 protein demonstrated at least some similarity to  
15 sequences identified as D45913 (leucine-rich-repeat protein [Mus musculus]) and M59472 (asparagine-rich antigen Pfa55-6 [Plasmodium falciparum]). Based upon sequence similarity, BD176\_3 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BD339\_1"

20 A polynucleotide of the present invention has been identified as clone "BD339\_1". BD339\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD339\_1 is a full-length clone, including the entire coding  
25 sequence of a secreted protein (also referred to herein as "BD339\_1 protein").

The nucleotide sequence of BD339\_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BD339\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD339\_1 should be approximately 650 bp.

The nucleotide sequence disclosed herein for BD339\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BD339\_1 demonstrated at least some similarity with sequences identified as H82422  
35 (yu80d08.s1 Homo sapiens cDNA clone 240111 3), N62058 (EST53c05 Homo sapiens cDNA

clone), U21730 Human 5'-nucleotidase (CD73)), W01979 (za30h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 294113 5'), and W02015 (za32b11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 294237 5'). Based upon sequence similarity, BD339\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII  
5 computer program predicts three potential transmembrane domains within the BD339\_1 protein sequence, centered around amino acids 14, 46, and 76 of SEQ ID NO:76, respectively.

#### Clone "BD427\_1"

A polynucleotide of the present invention has been identified as clone "BD427\_1".  
10 BD427\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD427\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD427\_1 protein").

15 The nucleotide sequence of BD427\_1 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BD427\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 BD427\_1 should be approximately 1810 bp.

The nucleotide sequence disclosed herein for BD427\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BD427\_1 demonstrated at least some similarity with sequences identified as BD427\_1 demonstrated at least some similarity with sequences identified as AA027122 (zk04a03.r1 Soares  
25 pregnant uterus NbHPU Homo sapiens cDNA clone 469516 5'), N24735 (yx56b02.s1 Homo sapiens cDNA clone 265707 3'), and W84644 (zd91a06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 356818 5'). Based upon sequence similarity, BD427\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BL229\_22"

30 A polynucleotide of the present invention has been identified as clone "BL229\_22". BL229\_22 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

acid sequence of the encoded protein. BL229\_22 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BL229\_22 protein").

The nucleotide sequence of the 5' portion of BL229\_22 as presently determined is reported in SEQ ID NO:79. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:80. The predicted amino acid sequence of the BL229\_22 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Additional nucleotide sequence from the 3' portion of BL229\_22, including a poly(A) tail, is reported in SEQ ID NO:81.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BL229\_22 should be approximately 870 bp.

The nucleotide sequence disclosed herein for BL229\_22 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "BV123\_16"

A polynucleotide of the present invention has been identified as clone "BV123\_16". BV123\_16 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV123\_16 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV123\_16 protein").

The nucleotide sequence of BV123\_16 as presently determined is reported in SEQ ID NO:82, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV123\_16 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:83.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV123\_16 should be approximately 1080 bp.

The nucleotide sequence disclosed herein for BV123\_16 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV123\_16 demonstrated at least some similarity with sequences identified as H29610 (ym61e03.s1 Homo sapiens cDNA clone 52653 3'), H52374 (yq81b12.r1 Homo sapiens cDNA clone 202175 5'), H66213 (yu16h10.s1 Homo sapiens cDNA), L08092 (Homo sapiens dystrophin (DMD) gene, intron 7, transposon-like sequence), L35670 (Homo sapiens (subclone H8 10\_g5 from P1 35 H5 C8) DNA sequence), M62716 (Human CSP-B gene flanking sequence), N46985 (yy83a05.s1 Homo sapiens cDNA clone 280112 3'), R94603 (yq38a04.s1 Homo sapiens

cDNA clone 198030 3'), U91321 (Human chromosome 16p13 BAC clone CIT987SK-363E6, complete sequence), and Z82200 (Human DNA sequence from clone J333E231). Based upon sequence similarity, BV123\_16 proteins and each similar protein or peptide may share at least some activity.

5

#### Clone "CH377\_1"

A polynucleotide of the present invention has been identified as clone "CH377\_1". CH377\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CH377\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CH377\_1 protein").

The nucleotide sequence of CH377\_1 as presently determined is reported in SEQ ID NO:84, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CH377\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:85. Amino acids 5 to 17 of SEQ ID NO:85 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CH377\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CH377\_1 should be approximately 570 bp.

The nucleotide sequence disclosed herein for CH377\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CH377\_1 demonstrated at least some similarity with sequences identified as AA507382 (nh73b01.s1 NCI\_CGAP\_Br1.1 Homo sapiens cDNA clone IMAGE 964105) and N70479 (za74f12.s1 Homo sapiens cDNA clone 298319 3'). Based upon sequence similarity, CH377\_1 proteins and each similar protein or peptide may share at least some activity.

30

#### Clone "BD441\_1"

A polynucleotide of the present invention has been identified as clone "BD441\_1". BD441\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

35

acid sequence of the encoded protein. BD441\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD441\_1 protein").

The nucleotide sequence of the 5' portion of BD441\_1 as presently determined is reported in SEQ ID NO:86. An additional internal nucleotide sequence from BD441\_1 as presently  
5 determined is reported in SEQ ID NO:87. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:88. Additional nucleotide sequence from the 3' portion of BD441\_1, including a poly(A) tail, is reported in SEQ ID NO:89.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
10 BD441\_1 should be approximately 2400 bp.

The predicted amino acid sequence disclosed herein for BD441\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BD441\_1 protein demonstrated at least some similarity to sequences identified as X61615 (leukemia inhibitory factor receptor [Homo sapiens]). Based upon sequence similarity,  
15 BD441\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BD441\_2"

A polynucleotide of the present invention has been identified as clone "BD441\_2". BD441\_2 was isolated from a human fetal kidney cDNA library using methods which are  
20 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD441\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD441\_2 protein").

The nucleotide sequence of the 5' portion of BD441\_2 as presently determined is reported  
25 in SEQ ID NO:90. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:91. The predicted amino acid sequence of the BD441\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:91. Additional nucleotide sequence from the 3' portion of BD441\_2, including a poly(A) tail, is reported in SEQ ID NO:92.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD441\_2 should be approximately 1200 bp.

The predicted amino acid sequence disclosed herein for BD441\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BD441\_2 protein demonstrated at least some similarity to sequences identified as

X61615 (leukemia inhibitory factor receptor [Homo sapiens]). Based upon sequence similarity, BD441\_2 proteins and each similar protein or peptide may share at least some activity.

Clone "BG102\_3"

5 A polynucleotide of the present invention has been identified as clone "BG102\_3". BG102\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG102\_3 is a full-length clone, including the entire coding sequence of  
10 a secreted protein (also referred to herein as "BG102\_3 protein").

The nucleotide sequence of BG102\_3 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG102\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 11 to 23 of SEQ ID  
15 NO:94 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BG102\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 BG102\_3 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for BG102\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG102\_3 demonstrated at least some similarity with sequences identified as AC002078 (Human BAC clone RG111H14 from 7q22, complete sequence), L11910 (Human  
25 retinoblastoma susceptibility gene exons 1-27, complete cds), U62317 (Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence), Z54147 (Human DNA sequence from cosmid L129H7, Huntington's Disease Region, chromosome 4p16.3 contains CpG island), Z75747 (Human DNA sequence from cosmid U96H1, between markers DXS366 and DXS87 on chromosome X \*), and Z80899 (Human DNA sequence from cosmid F1121 on chromosome 6).  
30 The predicted amino acid sequence disclosed herein for BG102\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG102\_3 protein demonstrated at least some similarity to sequences identified as M13100 (unknown protein [Rattus norvegicus]) and U15647 (reverse transcriptase [Mus musculus]). Based upon sequence similarity, BG102\_3 proteins and each similar protein or



peptide may share at least some activity. The nucleotide sequence of BG102\_3 indicates that it may contain an L1 repetitive element.

BG102\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 55 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "BK158\_1"

A polynucleotide of the present invention has been identified as clone "BK158\_1". BK158\_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BK158\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BK158\_1 protein").

The nucleotide sequence of BK158\_1 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BK158\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BK158\_1 should be approximately 1150 bp.

The nucleotide sequence disclosed herein for BK158\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BK158\_1 demonstrated at least some similarity with sequences identified as N39195 (yv26e08.s1 Homo sapiens cDNA clone 243878 3') and N45263 (yv26e08.r1 Homo sapiens cDNA clone 243878 5'). Based upon sequence similarity, BK158\_1 proteins and each similar protein or peptide may share at least some activity.

BK158\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 28 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "BP163\_1"

A polynucleotide of the present invention has been identified as clone "BP163\_1". BP163\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. BP163\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BP163\_1 protein").

The nucleotide sequence of the 5' portion of BP163\_1 as presently determined is reported in SEQ ID NO:97. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:98. The predicted amino acid sequence of the BP163\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Additional nucleotide sequence from the 3' portion of BP163\_1, including a poly(A) tail, is reported in SEQ ID NO:99.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BP163\_1 should be approximately 1240 bp.

The nucleotide sequence disclosed herein for BP163\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BP163\_1 demonstrated at least some similarity with sequences identified as AA187086 (zp58h06.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 624443 5' similar to TR G285943 G285943 ORF, COMPLETE CDS), AA301506 (EST14475 Testis tumor Homo sapiens cDNA 5' end similar to hypothetical protein (GB D14659)), D14659 (Human mRNA for KIAA0103 gene, complete cds), and W57328 (ma26d10.r1 Life Tech mouse brain Mus musculus cDNA clone). The predicted amino acid sequence disclosed herein for BP163\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BP163\_1 protein demonstrated at least some similarity to sequences identified as D14659 (KIAA0103 [Homo sapiens]). Based upon sequence similarity, BP163\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BZ16\_3"

A polynucleotide of the present invention has been identified as clone "BZ16\_3". BZ16\_3 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BZ16\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BZ16\_3 protein").

The partial nucleotide sequence of BZ16\_3, including its 3' end and a poly(A) tail, as presently determined is reported in SEQ ID NO:101. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:102. The predicted amino acid sequence of the BZ16\_3 protein corresponding to the foregoing nucleotide sequence is

reported in SEQ ID NO:102. Additional nucleotide sequence from the 5' portion of BZ16\_3 is reported in SEQ ID NO:100.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BZ16\_3 should be approximately 2120 bp.

5       The nucleotide sequence disclosed herein for BZ16\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BZ16\_3 demonstrated at least some similarity with sequences identified as F06886 (H. sapiens partial cDNA sequence; clone c-1nf02), F06870 (H. sapiens partial cDNA sequence; clone c-1nc11), N53511 (yz26b08.s1 Homo sapiens cDNA clone 284151 3'), T65313 (yc79g12.s1  
10 Homo sapiens cDNA clone 22132 3'), U00084 (Haemophilus influenzae), W44815 (zc21d01.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 322945 3'), and Z49128 (Caenorhabditis elegans cosmid M03C11). The predicted amino acid sequence disclosed herein for BZ16\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BZ16\_3 protein demonstrated at least some  
15 similarity to sequences identified as D26185 (cell division protein [Bacillus subtilis]), L46096 (HEAH11465\_1 cell division protein [Haemophilus influenzae]), and Z49128 (CEM03C11\_5 M03C11.5 [Caenorhabditis elegans]). The BZ16\_3 protein demonstrated at least some similarity to ATP-dependent proteases such as ftsH. Based upon sequence similarity, BZ16\_3 proteins and each similar protein or peptide may share at least some activity.

20

#### Clone "CC182\_1"

A polynucleotide of the present invention has been identified as clone "CC182\_1". CC182\_1 was isolated from a human adult brain cDNA library using methods which are selective  
25 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CC182\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC182\_1 protein").

The nucleotide sequence of CC182\_1 as presently determined is reported in SEQ ID  
30 NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CC182\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104. Amino acids 26 to 38 of SEQ ID NO:104 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 39. Due to the hydrophobic nature of the predicted leader/signal

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CC182\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CC182\_1 should be approximately 1600 bp.

5       The nucleotide sequence disclosed herein for CC182\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CC182\_1 demonstrated at least some similarity with sequences identified as H61159 (yu37f08.s1 Homo sapiens cDNA clone 236007 3' similar to contains L1 repetitive element), L09709 (Human lysosomal-associated membrane glycoprotein-2 (LAMP2) gene, 5' end of CDS and flanking region), W44797 (zb98e10.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320874 3' similar to contains Alu repetitive element), and X62167 (H.sapiens mRNA for P2 protein of peripheral myelin). Based upon sequence similarity, CC182\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CC182\_1 indicates that it may contain an L1 repetitive element and/or a MER42C repetitive element.

15

#### Clone "CG109\_1"

A polynucleotide of the present invention has been identified as clone "CG109\_1". CG109\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CG109\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CG109\_1 protein").

20       The nucleotide sequence of CG109\_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CG109\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

25       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CG109\_1 should be approximately 600 bp.

30       The nucleotide sequence disclosed herein for CG109\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

#### Clone "CJ397\_1"

A polynucleotide of the present invention has been identified as clone "CJ397\_1". CJ397\_1 was isolated from a human fetal brain cDNA library using methods which are selective

35

for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ397\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ397\_1 protein").

5       The nucleotide sequence of the 5' portion of CJ397\_1 as presently determined is reported in SEQ ID NO:107. An additional internal nucleotide sequence from CJ397\_1 as presently determined is reported in SEQ ID NO:108. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:109. Additional nucleotide sequence from the 3' portion of CJ397\_1, including a poly(A)  
10 tail, is reported in SEQ ID NO:110.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ397\_1 should be approximately 1900 bp.

The nucleotide sequence disclosed herein for CJ397\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
15 protocols. CJ397\_1 demonstrated at least some similarity with sequences identified as H18685 (yn52b08.s1 Homo sapiens cDNA clone 172023 3'), H46001 (yo13f06.s1 Homo sapiens cDNA clone 177827 3'), and T77612 (yc91f06.r1 Homo sapiens cDNA clone 23298 5'). Based upon sequence similarity, CJ397\_1 proteins and each similar protein or peptide may share at least some activity.

20

#### Clone "AM795\_4"

A polynucleotide of the present invention has been identified as clone "AM795\_4". AM795\_4 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified  
25 as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AM795\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AM795\_4 protein").

The nucleotide sequence of AM795\_4 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
30 frame and the predicted amino acid sequence of the AM795\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 9 to 21 of SEQ ID NO:112 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Amino acids 138 to 150 of SEQ ID NO:112 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid  
35 151. Due to the hydrophobic nature of the predicted and the possible leader/signal sequences,

each of such sequences may act as a transmembrane domain should that leader/signal sequence not be separated from the remainder of the AM795\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AM795\_4 should be approximately 1900 bp.

5       The nucleotide sequence disclosed herein for AM795\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AM795\_4 demonstrated at least some similarity with sequences identified as AF002700 (Homo sapiens GDNF family receptor alpha 2 (GFRalpha2) mRNA, complete cds), H05619 (yl70a10.s1 Homo sapiens cDNA clone 43207 3'), U46493 (Cloning vector pFlp recombina

10       se gene, complete cds), U59486 (Rattus norvegicus GDNF receptor alpha mRNA, complete cds), V00248 (Human Ret ligand retL2 cDNA), W73633 (zd55h01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344593 3', mRNA sequence), and W73681 (zd55h01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344593 5', mRNA sequence). The predicted amino acid sequence disclosed herein for AM795\_4 was searched against the GenPept

15       and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AM795\_4 protein demonstrated at least some similarity to sequences identified as AF002700 (GDNF family receptor alpha 2 (GFRalpha2) [Homo sapiens]), U59486 (GDNF receptor alpha [Rattus norvegicus]), and W37460 (Human Ret ligand retL2 cDNA). A receptor complex comprised of TrnR1 (GDNFR alpha) and Ret was found to be capable of mediating both GDNF

20       and NTN signaling. The receptor called TrnR2, identified based on homology to TrnR1, is 48% identical to TrnR1 and is encoded by a gene located on the short arm of chromosome 8. TrnR2 is attached to the cell surface via a GPI-linkage, and can mediate both NTN and GDNF signaling through Ret *in vitro* (Baloh *et al.*, 1997, *Neuron* 18(5): 793-802, which is incorporated by reference herein). Based upon sequence similarity, AM795\_4 proteins and each similar protein

25       or peptide may share at least some activity.

AM795\_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 76 kDa was detected in conditioned media fractions using SDS polyacrylamide gel electrophoresis.

30       Clone "AT340\_1"

A polynucleotide of the present invention has been identified as clone "AT340\_1". AT340\_1 was isolated from a human adult blood (lymphocytes and dendritic cells treated with mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or

35       transmembrane protein on the basis of computer analysis of the amino acid sequence of the

encoded protein. AT340\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AT340\_1 protein").

The partial nucleotide sequence of AT340\_1, including its 3' end and a poly(A) tail, as presently determined is reported in SEQ ID NO:114. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:115. The predicted amino acid sequence of the AT340\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:115. Amino acids 12 to 24 of SEQ ID NO:115 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AT340\_1 protein. Additional nucleotide sequence from the 5' portion of AT340\_1 is reported in SEQ ID NO:113.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AT340\_1 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for AT340\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AT340\_1 demonstrated at least some similarity with sequences identified as AA039343 (zk39g04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 485238 3'), R68951 (yi43g06.r1 Homo sapiens cDNA clone 142042 5' similar to SP:C35D10.1 CE01190), R77532 (yi76c01.r1 Homo sapiens cDNA), R92619 (yq04a04.r1 Homo sapiens cDNA clone 195918 5' similar to SP:C35D10.1 CE01190), and W60997 (zc99f09.s1 Pancreatic Islet Homo sapiens cDNA clone 339305 3'). The predicted amino acid sequence disclosed herein for AT340\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AT340\_1 protein demonstrated at least some similarity to sequences identified as U21324 (similar to *S. cerevisiae* hypothetical protein YKL166 [*Caenorhabditis elegans*]). Based upon sequence similarity, AT340\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BG132\_1"

A polynucleotide of the present invention has been identified as clone "BG132\_1". BG132\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG132\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG132\_1 protein").

The nucleotide sequence of the 5' portion of BG132\_1 as presently determined is reported in SEQ ID NO:116. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:117. The predicted amino acid sequence of the BG132\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:117.

- 5 Amino acids 121 to 133 of SEQ ID NO:117 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 134. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BG132\_1 protein. Additional nucleotide sequence from the 3' portion of BG132\_1, including a poly(A) tail,  
10 is reported in SEQ ID NO:118.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG132\_1 should be approximately 2000 bp.

- The nucleotide sequence disclosed herein for BG132\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
15 protocols. BG132\_1 demonstrated at least some similarity with sequences identified as AA078587 (7P05H12 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P05H12), H14301 (ym63c04.rl Homo sapiens cDNA clone 163590 5' similar to gb:U03642\_cds1 PROBABLE G PROTEIN-COUPLED RECEPTOR APJ (HUMAN)), L09249 (putative G-protein coupled receptor, rhodopsin family), S79811 (adrenomedullin receptor [rats,  
20 lung, mRNA]), T36034 (rchd523 gene differentially expressed in cardiovascular disease), U58828 (Human IL8-related receptor (DRY12) mRNA, complete cds), and Y08162 (H.sapiens mRNA for heptahelix receptor). The predicted amino acid sequence disclosed herein for BG132\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG132\_1 protein demonstrated at least some similarity to  
25 sequences identified as L06109 (G protein-coupled receptor [Gallus gallus]), L34339 (galanin receptor [Homo sapiens]), U30290 (galanin receptor GALR1 [Rattus norvegicus]), U58828 (IL8-related receptor [Homo sapiens]), W03739 (rchd523 gene product (G protein-coupled receptor)), X98510 (G protein-coupled receptor [Homo sapiens]), and Y08162 (heptahelix receptor [Homo sapiens]). Based upon sequence similarity, BG132\_1 proteins and each similar  
30 protein or peptide may share at least some activity.

#### Clone "BG219\_2"

- A polynucleotide of the present invention has been identified as clone "BG219\_2". BG219\_2 was isolated from a human adult brain cDNA library using methods which are selective  
35 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding



a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG219\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG219\_2 protein").

5 The nucleotide sequence of BG219\_2 as presently determined is reported in SEQ ID NO:119, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG219\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:120.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG219\_2 should be approximately 700 bp.

10 The nucleotide sequence disclosed herein for BG219\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG219\_2 demonstrated at least some similarity with sequences identified as AA210695 (zr88b05.s1 Soares NbHTGBC Homo sapiens cDNA clone 682737 3'), C01459 (HUMGS0008450, Human Gene Signature, 3'-directed cDNA sequence), N22628 (EST49p115  
15 Homo sapiens cDNA clone 49p115), and T26211 (Human gene signature HUMGS08450). Based upon sequence similarity, BG219\_2 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BG366\_2"

20 A polynucleotide of the present invention has been identified as clone "BG366\_2". BG366\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG366\_2 is a full-length clone, including the entire coding sequence of  
25 a secreted protein (also referred to herein as "BG366\_2 protein").

The nucleotide sequence of BG366\_2 as presently determined is reported in SEQ ID NO:121, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG366\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:122. The amino acid sequence of  
30 another protein that could be encoded by BG366\_2 is reported in SEQ ID NO:283.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG366\_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BG366\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
35 protocols. BG366\_2 demonstrated at least some similarity with sequences identified as N39453

(yy49h03.s1 Homo sapiens cDNA clone 276917 3'). Based upon sequence similarity, BG366\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the BG366\_2 protein sequence centered around amino acid 92 of SEQ ID NO:122.

5

Clone "BV172\_2"

A polynucleotide of the present invention has been identified as clone "BV172\_2". BV172\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
10 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV172\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV172\_2 protein").

The nucleotide sequence of BV172\_2 as presently determined is reported in SEQ ID NO:123, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
15 frame and the predicted amino acid sequence of the BV172\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:124.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV172\_2 should be approximately 1650 bp.

The nucleotide sequence disclosed herein for BV172\_2 was searched against the GenBank  
20 and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV172\_2 demonstrated at least some similarity with sequences identified as No significant hits were found in the database. The TopPredII computer program predicts a potential transmembrane domain within the BV172\_2 protein sequence centered around amino acid 19 of SEQ ID NO:124. The nucleotide sequence of BV172\_2 indicates that it may contain one or more  
25 of the following types of repetitive elements: an element similar to chicken CR1, human L1, Mer33.

30

Clone "CC247\_10"

A polynucleotide of the present invention has been identified as clone "CC247\_10". CC247\_10 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

acid sequence of the encoded protein. CC247\_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC247\_10 protein").

The nucleotide sequence of CC247\_10 as presently determined is reported in SEQ ID NO:125, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
5 frame and the predicted amino acid sequence of the CC247\_10 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:126. Amino acids 1 to 8 of SEQ ID NO:126 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 9. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be  
10 separated from the remainder of the CC247\_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CC247\_10 should be approximately 550 bp.

The nucleotide sequence disclosed herein for CC247\_10 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA  
15 search protocols. CC247\_10 demonstrated at least some similarity with sequences identified as AA291226 (zs47d03.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone 700613 5'), T05738 (EST03627 Homo sapiens cDNA clone HFBDF64), W51195 (ma14b04.r1 Life Tech mouse brain Mus musculus cDNA clone 304495 5'), and W93640 (zd95d09.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 357233 3'). The predicted amino acid sequence disclosed herein for  
20 CC247\_10 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CC247\_10 protein demonstrated at least some similarity to sequences identified as M62424 (thrombin receptor [Homo sapiens]). The predicted CC247\_10 protein is highly hydrophobic. Based upon sequence similarity, CC247\_10 proteins and each similar protein or peptide may share at least some activity.

25

#### Clone "CI480\_9"

A polynucleotide of the present invention has been identified as clone "CI480\_9". CI480\_9 was isolated from a human adult brain cDNA library using methods which are selective  
30 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CI480\_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CI480\_9 protein").

The nucleotide sequence of CI480\_9 as presently determined is reported in SEQ ID  
35 NO:127, and includes a poly(A) tail. What applicants presently believe to be the proper reading

frame and the predicted amino acid sequence of the CI480\_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:128. Amino acids 39 to 51 of SEQ ID NO:128 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 52. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CI480\_9 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CI480\_9 should be approximately 1940 bp.

The nucleotide sequence disclosed herein for CI480\_9 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CI480\_9 demonstrated at least some similarity with sequences identified as N99342 (IMAGE:20093 Homo sapiens cDNA clone 20093), R89725 (ym99d09.r1 Homo sapiens cDNA clone 167057 5'), and U60644 (Human HU-K4 mRNA, complete cds). The predicted amino acid sequence disclosed herein for CI480\_9 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CI480\_9 protein demonstrated at least some similarity to sequences identified as U60644 (HU-K4 [Homo sapiens]). Based upon sequence similarity, CI480\_9 proteins and each similar protein or peptide may share at least some activity.

CI480\_9 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 63 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "CO722\_1"

A polynucleotide of the present invention has been identified as clone "CO722\_1". CO722\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO722\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO722\_1 protein").

The nucleotide sequence of CO722\_1 as presently determined is reported in SEQ ID NO:129, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO722\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:130. Amino acids 17 to 29 of SEQ ID NO:130 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CO722\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO722\_1 should be approximately 6800 bp.

5       The nucleotide sequence disclosed herein for CO722\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO722\_1 demonstrated at least some similarity with sequences identified as AA186616 (zp71a08.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 625622 3' similar to contains Alu repetitive element), H10376 (ym08a03.s1 Homo sapiens cDNA clone  
10 47067 3'), N86013 (J5997F Fetal heart, Lambda ZAP Express Homo sapiens cDNA), U55258 (Human hBRAVO/Nr-CAM precursor (hBRAVO/ Nr-CAM) gene, complete cds), W19770 (zb39d01.r1 Soares parathyroid tumor NbHPA Homo sapiens), W31608 (zb91d09.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone), and X58482 (Chicken mRNA for neuronal transmembrane protein Nr-CAM, ng-CAM related). The predicted amino acid sequence  
15 disclosed herein for CO722\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CO722\_1 protein demonstrated at least some similarity to sequences identified as AB002341 (KIAA0343 [Homo sapiens]) and X58482 (Nr-CAM protein [Gallus gallus]). Based upon sequence similarity, CO722\_1 proteins and each similar protein or peptide may share at least some activity. The  
20 TopPredII computer program predicts two potential transmembrane domains within the CO722\_1 protein sequence, centered around amino acids 610 and 1070 of SEQ ID NO:130, respectively.

CO722\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 160 kDa was detected in conditioned media fractions using SDS polyacrylamide gel electrophoresis.

25

#### Clone "CT748\_2"

A polynucleotide of the present invention has been identified as clone "CT748\_2". CT748\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
30 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CT748\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT748\_2 protein").

The nucleotide sequence of CT748\_2 as presently determined is reported in SEQ ID NO:131, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
35 frame and the predicted amino acid sequence of the CT748\_2 protein corresponding to the

foregoing nucleotide sequence is reported in SEQ ID NO:132. Amino acids 281 to 293 of SEQ ID NO:132 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 294. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CT748\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT748\_2 should be approximately 5500 bp.

The nucleotide sequence disclosed herein for CT748\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CT748\_2 demonstrated at least some similarity with sequences identified as T48063 (yb24f03.s1 Homo sapiens cDNA clone 72125 3') and X54175 (Human specific Alu element (HS C4N2) DNA). The predicted amino acid sequence disclosed herein for CT748\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CT748\_2 protein demonstrated at least some similarity to sequences identified as Z36714 (cyclin F [Homo sapiens]). Based upon sequence similarity, CT748\_2 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CT748\_2 indicates that it may contain an Alu repetitive element.

#### Clone "AJ1\_1"

A polynucleotide of the present invention has been identified as clone "AJ1\_1". AJ1\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AJ1\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AJ1\_1 protein").

The nucleotide sequence of the 5' portion of AJ1\_1 as presently determined is reported in SEQ ID NO:133. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:134. The predicted amino acid sequence of the AJ1\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:134. Additional nucleotide sequence from the 3' portion of AJ1\_1, including a poly(A) tail, is reported in SEQ ID NO:135.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AJ1\_1 should be approximately 925 bp.

The predicted amino acid sequence disclosed herein for AJ1\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The

predicted AJ1\_1 protein demonstrated at least some similarity to sequences identified as U39060 (GRIP1 [Mus musculus]). Based upon sequence similarity, AJ1\_1 proteins and each similar protein or peptide may share at least some activity.

5        Clone "AQ73\_3"

A polynucleotide of the present invention has been identified as clone "AQ73\_3". AQ73\_3 was isolated from a human adult ovary (PA-1 teratocarcinoma, untreated tissue pooled with retinoic-acid-treated and activin-treated tissue) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified  
10 as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AQ73\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AQ73\_3 protein").

The nucleotide sequence of AQ73\_3 as presently determined is reported in SEQ ID NO:136, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
15 frame and the predicted amino acid sequence of the AQ73\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:137.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AQ73\_3 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for AQ73\_3 was searched against the GenBank  
20 and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AQ73\_3 demonstrated at least some similarity with sequences identified as AA514474 (nf57g01.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone 924048), T47520 (Human hepatoma-derived growth factor (HDGF-2) cDNA), W24708 (zb62e08.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 308198 5'), and W45513 (zc27g08.s1 Soares senescent  
25 fibroblasts NbHSF Homo sapiens cDNA clone 323582 3'). The predicted amino acid sequence disclosed herein for AQ73\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AQ73\_3 protein demonstrated at least some similarity to sequences identified as D16431 (hepatoma-derived GF [Homo sapiens]), D63707 (mouse hepatoma derived growth factor (HDGF) [Mus musculus]), R66727 (Human  
30 hepatoma derived growth factor), U18997 (ORF\_f299 [Escherichia coli]), U97193 (similar to S. cerevisiae SIR2 (SP P06700) and mouse hepatoma derived growth factor HDGF (NID g945418) [Caenorhabditis elegans]), and W09404 (Human hepatoma-derived growth factor (HDGF-2)). Based upon sequence similarity, AQ73\_3 proteins and each similar protein or peptide may share at least some activity.

AQ73\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 67 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5        Clone "BG142\_1"

A polynucleotide of the present invention has been identified as clone "BG142\_1". BG142\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG142\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG142\_1 protein").

The nucleotide sequence of BG142\_1 as presently determined is reported in SEQ ID NO:138, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG142\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:139.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG142\_1 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for BG142\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG142\_1 demonstrated at least some similarity with sequences identified as AA170261 (ms87h11.r1 Soares mouse 3NbMS Mus musculus cDNA clone 618597 5' similar to TR E245601 E245601 G-RICH BOX-BINDING PROTEIN), L04282 (Human CACCC box-binding protein mRNA, complete cds), N27696 (yx51h12.r1 Homo sapiens cDNA clone 265319 5'), W96110 (ze09a11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358460 5'), and W96111 (ze09a11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358460 3'). The predicted amino acid sequence disclosed herein for BG142\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG142\_1 protein demonstrated at least some similarity to sequences identified as U80078 (transcription factor BFCOL1 [Mus musculus]) and X98096 (G-rich box-binding protein [Mus musculus]). Based upon sequence similarity, BG142\_1 proteins and each similar protein or peptide may share at least some activity.

30        Clone "BV66\_1"

A polynucleotide of the present invention has been identified as clone "BV66\_1". BV66\_1 was isolated from a human adult brain cDNA library using methods which are selective



for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV66\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV66\_1 protein").

5       The nucleotide sequence of BV66\_1 as presently determined is reported in SEQ ID NO:140, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV66\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:141.

10       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV66\_1 should be approximately 870 bp.

      The nucleotide sequence disclosed herein for BV66\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The nucleotide sequence of BV66\_1 indicates that it may contain a TAAA1 simple repeat element.

15

Clone "BV291\_3"

      A polynucleotide of the present invention has been identified as clone "BV291\_3". BV291\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
20       a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV291\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV291\_3 protein").

      The nucleotide sequence of BV291\_3 as presently determined is reported in SEQ ID NO:142, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
25       frame and the predicted amino acid sequence of the BV291\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:143.

      The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV291\_3 should be approximately 2000 bp.

      The nucleotide sequence disclosed herein for BV291\_3 was searched against the GenBank  
30       and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV291\_3 demonstrated at least some similarity with sequences identified as H10954 (ym06e09.r1 Homo sapiens cDNA clone 47034 5'), H10955 (ym06e09.s1 Homo sapiens cDNA clone 47034 3'), N25300 (yw52c10.s1 Homo sapiens cDNA clone 255858 3'), T25940 (Human gene signature HUMGS08173), T68890 (yc30g11.s1 Homo sapiens cDNA clone 82244 3'),  
35       T78286 (yc99a08.r1 Homo sapiens cDNA clone 24033 5'), Z39987 (H. sapiens partial cDNA

sequence; clone c-1oh05), and Z47073 (Caenorhabditis elegans cosmid ZC506). The predicted amino acid sequence disclosed herein for BV291\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BV291\_3 protein demonstrated at least some similarity to sequences identified as X02155 (BTTGR\_1 thyroglobulin [Bos taurus]). Based upon sequence similarity, BV291\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the BV291\_3 protein sequence centered around amino acid 48 of SEQ ID NO:143.

BV291\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 30 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "CK201\_1"

A polynucleotide of the present invention has been identified as clone "CK201\_1". CK201\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CK201\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CK201\_1 protein").

The nucleotide sequence of CK201\_1 as presently determined is reported in SEQ ID NO:144, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CK201\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:145.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CK201\_1 should be approximately 1080 bp.

The nucleotide sequence disclosed herein for CK201\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CK201\_1 demonstrated at least some similarity with sequences identified as AA129133 (zo09h12.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 567239 3' similar to contains Alu repetitive element), D81444 (Human fetal brain cDNA 5'-end GEN-164G10), R36326 (yg69h09.r1 Homo sapiens cDNA clone 38821 5'), T08553 (Oncogene R-ras mutant cDNA (exons 2-6)), T31595 (Probe (BLUR13) for Alu repeat sequence), X03273 (Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene), and X69907 (H.sapiens gene for mitochondrial ATP synthase c subunit). The predicted amino acid sequence disclosed herein for CK201\_1 was searched against the GenPept and GeneSeq amino acid

sequence databases using the BLASTX search protocol. The predicted CK201\_1 protein demonstrated at least some similarity to sequences identified as D21827 (major surface glycoprotein [*Pneumocystis carinii*]). Based upon sequence similarity, CK201\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of

5 CK201\_1 indicates that it may contain an Alu repetitive element.

CK201\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 40 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

10 Clone "CQ331\_2"

A polynucleotide of the present invention has been identified as clone "CQ331\_2". CQ331\_2 was isolated from a human adult heart cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

15 of the encoded protein. CQ331\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CQ331\_2 protein").

The nucleotide sequence of CQ331\_2 as presently determined is reported in SEQ ID NO:146, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CQ331\_2 protein corresponding to the

20 foregoing nucleotide sequence is reported in SEQ ID NO:147. Amino acids 7 to 19 of SEQ ID NO:147 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CQ331\_2 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CQ331\_2 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for CQ331\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CQ331\_2 demonstrated at least some similarity with sequences identified as J03766

30 (Canine cardiac calsequestrin mRNA, complete cds), L29766 (Homo sapiens epoxide hydrolase (EPHX) gene, complete cds), N83601 (KK1173F Homo sapiens cDNA clone KK1173 5' similar to CALSEQUESTRIN (CARDIAC)), T99646 (ye73f12.s1 Homo sapiens cDNA clone 123407 3' similar to contains Alu repetitive element;contains PTR5 repetitive element), and W76326 (zd60d04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 345031 5' similar to

35 contains Alu repetitive element). The predicted amino acid sequence disclosed herein for

CQ331\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CQ331\_2 protein demonstrated at least some similarity to sequences identified as J03766 (DOGCAL\_1 Canine cardiac calsequestrin mRNA, complete cds [Canis canis]) and X55040 (calsequestrin [Oryctolagus cuniculus]). Based upon  
5 sequence similarity, CQ331\_2 proteins and each similar protein or peptide may share at least some activity.

#### Clone "CT550\_1"

A polynucleotide of the present invention has been identified as clone "CT550\_1".  
10 CT550\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CT550\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT550\_1 protein").

15 The nucleotide sequence of CT550\_1 as presently determined is reported in SEQ ID NO:148, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CT550\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:149.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 CT550\_1 should be approximately 1070 bp.

The nucleotide sequence disclosed herein for CT550\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The TopPredII computer program predicts a potential transmembrane domain within the CT550\_1 protein sequence centered around amino  
25 acid 25 of SEQ ID NO:149.

CT550\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 7 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### 30 Clone "CT585\_1"

A polynucleotide of the present invention has been identified as clone "CT585\_1". CT585\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. CT585\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT585\_1 protein").

The nucleotide sequence of CT585\_1 as presently determined is reported in SEQ ID NO:150, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
5 frame and the predicted amino acid sequence of the CT585\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:151. Amino acids 2 to 14 of SEQ ID NO:151 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal  
10 sequence not be separated from the remainder of the CT585\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT585\_1 should be approximately 2710 bp.

The nucleotide sequence disclosed herein for CT585\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
15 protocols. CT585\_1 demonstrated at least some similarity with sequences identified as AA069442 (zf74b02.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone 382635 3'), L38961 (Homo sapiens putative transmembrane protein (B5) mRNA, complete cds), N34932 (yy49b10.s1 Homo sapiens cDNA clone 276859 3'), N60101 (TgESTzy11f10.r1 Toxoplasma gondii cDNA clone tgzy11f10.r1 5'), and U13019 (Caenorhabditis elegans cosmid T12A2). The predicted amino acid  
20 sequence disclosed herein for CT585\_1 was searched against the GenPept, GeneSeq, and SwissProt amino acid sequence databases using the BLASTX search protocol. The predicted CT585\_1 protein demonstrated at least some similarity to sequences identified as L34260 (transmembrane protein [Mus musculus]), L38961 (transmembrane protein [Homo sapiens]), P46975 (Caenorhabditis elegans oligosaccharyl transferase stt3 [Caenorhabditis elegans]), and  
25 U13019 (Caenorhabditis elegans cosmid T12A2 [Caenorhabditis elegans]). Based upon sequence similarity, CT585\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "CT797\_3"

A polynucleotide of the present invention has been identified as clone "CT797\_3".  
30 CT797\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CT797\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT797\_3 protein").

The nucleotide sequence of CT797\_3 as presently determined is reported in SEQ ID NO:152, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CT797\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:153.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT797\_3 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for CT797\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CT797\_3 demonstrated at least some similarity with sequences identified as AA573847  
10 (nk08d06.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA clone IMAGE:1012907). The predicted amino acid sequence disclosed herein for CT797\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CT797\_3 protein demonstrated at least some similarity to sequences identified as U18309 (chromokinesin [Gallus gallus]) and Z82271 (T01G1.1 [Caenorhabditis elegans]). Based upon  
15 sequence similarity, CT797\_3 proteins and each similar protein or peptide may share at least some activity.

CT797\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 80 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

20

#### Clone "CB107\_1"

A polynucleotide of the present invention has been identified as clone "CB107\_1". CB107\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
25 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CB107\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CB107\_1 protein").

The nucleotide sequence of the 5' portion of CB107\_1 as presently determined is reported in SEQ ID NO:154. An additional internal nucleotide sequence from CB107\_1 as presently  
30 determined is reported in SEQ ID NO:155. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:156. Additional nucleotide sequence from the 3' portion of CB107\_1, including a poly(A) tail, is reported in SEQ ID NO:157.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
35 CB107\_1 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for CB107\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CB107\_1 demonstrated at least some similarity with sequences identified as AA121485 (zn80a02.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 564458 3'),  
5 AA428192 (zw51b08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773559 3'), D83018 (Human mRNA for nel-related protein 2, complete cds), F10919 (H. sapiens partial cDNA sequence; clone c-3lg01), H15375 (ym28d09.r1 Homo sapiens cDNA clone 49527 5' similar to SP A54105 A54105 FIBRILLIN-2 PRECURSOR), U48245 (Rattus norvegicus protein kinase C-binding protein Nel mRNA, complete cds), U59230 (Mus musculus mel (MEL91)  
10 mRNA, complete cds), and W28387 (46c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA). The predicted amino acid sequence disclosed herein for CB107\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CB107\_1 protein demonstrated at least some similarity to sequences identified as D83018 (nel-related protein 2 [Homo sapiens]), R05222 (Antigen  
15 GX5401FL encoded by Eimeria tenella genomic DNA), R79964 (Connective tissue growth factor), U48245 (RNU48245\_1 protein kinase C-binding protein Nel [Rattus norvegicus]), and U59230 (mel [Mus musculus]). Based upon sequence similarity, CB107\_1 proteins and each similar protein or peptide may share at least some activity.

20

#### Clone "CG300\_3"

A polynucleotide of the present invention has been identified as clone "CG300\_3". CG300\_3 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
25 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CG300\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CG300\_3 protein").

The nucleotide sequence of CG300\_3 as presently determined is reported in SEQ ID NO:158, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
30 frame and the predicted amino acid sequence of the CG300\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:159. Amino acids 30 to 42 of SEQ ID NO:159 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal  
35 sequence not be separated from the remainder of the CG300\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CG300\_3 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for CG300\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CG300\_3 demonstrated at least some similarity with sequences identified as N40185 (yy44d08.s1 Homo sapiens cDNA clone 276399 3') and W01791 (za72d06.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 298091 5'). Based upon sequence similarity, CG300\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the CG300\_3 protein sequence, centered around amino acids 34, 98, 151, and 179 of SEQ ID NO:159, respectively.

CG300\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 29 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "CJ145\_1"

A polynucleotide of the present invention has been identified as clone "CJ145\_1". CJ145\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ145\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ145\_1 protein").

The nucleotide sequence of CJ145\_1 as presently determined is reported in SEQ ID NO:160, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CJ145\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:161. Amino acids 6 to 18 of SEQ ID NO:161 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CJ145\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ145\_1 should be approximately 3600 bp.

The nucleotide sequence disclosed herein for CJ145\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search



protocols. CJ145\_1 demonstrated at least some similarity with sequences identified as R43655 (yc86b04.s1 Homo sapiens cDNA clone 22829 3'), R50995 (yg63f06.s1 Homo sapiens cDNA clone 37377 3' similar to contains MER22 repetitive element), and W92748 (zd92h03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 356981 3'). Based upon sequence similarity, CJ145\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CJ145\_1 indicates that it may contain a CA simple repeat element.

#### Clone "CJ160\_11"

A polynucleotide of the present invention has been identified as clone "CJ160\_11". CJ160\_11 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ160\_11 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ160\_11 protein").

The nucleotide sequence of CJ160\_11 as presently determined is reported in SEQ ID NO:162, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CJ160\_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:163. Amino acids 17 to 29 of SEQ ID NO:163 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CJ160\_11 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ160\_11 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for CJ160\_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CJ160\_11 demonstrated at least some similarity with sequences identified as AA024511 (ze76e04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364926 3') and AC000074 (00884; HTGS phase 3, complete sequence). Based upon sequence similarity, CJ160\_11 proteins and each similar protein or peptide may share at least some activity.

CJ160\_11 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 96 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "CO20\_1"

A polynucleotide of the present invention has been identified as clone "CO20\_1". CO20\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO20\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO20\_1 protein").

The nucleotide sequence of the 5' portion of CO20\_1 as presently determined is reported in SEQ ID NO:164. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:165. The predicted amino acid sequence of the CO20\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:165. Amino acids 17 to 29 of SEQ ID NO:165 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CO20\_1 protein. Additional nucleotide sequence from the 3' portion of CO20\_1, including a poly(A) tail, is reported in SEQ ID NO:166.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO20\_1 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for CO20\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO20\_1 demonstrated at least some similarity with sequences identified as AA045770 (zl68b10.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 509755 3' similar to SW:R13A\_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A), AA070899 (zm66c01.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 530592 3' similar to contains Alu repetitive element), AA325205 (EST28155 Cerebellum II Homo sapiens cDNA 5' end), N22253 (yw36a08.s1 Homo sapiens cDNA clone 254294 3' similar to SP S29539 S29539 BASIC PROTEIN, 23K), R01933 (ye85g07.s1 Homo sapiens cDNA clone 124572 3' similar to SP:S29539 S29539 BASIC PROTEIN, 23K), R12008 (yf51f04.r1 Homo sapiens cDNA clone 25456 5'), R39848 (yf51f04.s1 Homo sapiens cDNA clone 25456 3' similar to contains Alu repetitive element;contains PTR5 repetitive element), R56565 (yg91c12.r1 Homo sapiens cDNA clone 40891 5'), T19487 (Human gene signature HUMGS00543), T30988 (EST25695 Homo sapiens cDNA 5' end similar to None), U37026 (Rattus norvegicus brain sodium channel beta 2 subunit (SCNB2) mRNA, complete cds), and X56932 (H.sapiens mRNA for 23 kD highly basic protein). The predicted amino acid sequence disclosed herein for CO20\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

The predicted CO20\_1 protein demonstrated at least some similarity to sequences identified as U37026 (sodium channel beta 2 subunit [Rattus norvegicus]), U58658 (unknown [Homo sapiens]), and X56932 (23 kD highly basic protein [Homo sapiens]). The sodium channel beta 2 subunit is a glycoprotein with an extracellular domain containing an immunoglobulin-like fold with  
5 similarity to the neural cell adhesion molecule contactin. Based upon sequence similarity, CO20\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CO20\_1 indicates that it may contain an Alu repetitive element.

Clone "CO223\_3"

10 A polynucleotide of the present invention has been identified as clone "CO223\_3". CO223\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO223\_3 is a full-length clone, including the entire coding sequence of  
15 a secreted protein (also referred to herein as "CO223\_3 protein").

The nucleotide sequence of CO223\_3 as presently determined is reported in SEQ ID NO:167, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO223\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:168. Amino acids 35 to 47 of SEQ ID  
20 NO:168 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 48. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CO223\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 CO223\_3 should be approximately 700 bp.

The nucleotide sequence disclosed herein for CO223\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO223\_3 demonstrated at least some similarity with sequences identified as AA004498 (zh87b06.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 428243  
30 5' similar to gb M62505 C5A ANAPHYLATOXIN CHEMOTACTIC RECEPTOR (HUMAN); contains L1.t1 L1 repetitive element) and U47924 (Human chromosome 12p13 gene cluster, surface antigen CD4 (CD4), A, B, G-protein beta-3 subunit (GNB3), isopeptidase T (ISOT) and triosephosphate isomerase (TPI) genes, complete cds). Based upon sequence similarity, CO223\_3 proteins and each similar protein or peptide may share at least some activity.

The 3' end of the CO223\_3 polynucleotide sequence contains a 54-bp sequence that is repeated three times in the clone; these repeats begin at positions 314, 368, and 422 of SEQ ID NO:167 and encode amino acids 47 to 64, 65 to 82, and 83 to 99 of SEQ ID NO:168, respectively.

5        Clone "CO310\_2"

A polynucleotide of the present invention has been identified as clone "CO310\_2". CO310\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO310\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO310\_2 protein").

The nucleotide sequence of CO310\_2 as presently determined is reported in SEQ ID NO:169, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO310\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:170.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO310\_2 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for CO310\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The nucleotide sequence of CO310\_2 indicates that it may contain an L1 repetitive element.

Clone "CP258\_3"

A polynucleotide of the present invention has been identified as clone "CP258\_3". CP258\_3 was isolated from a human adult salivary gland cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CP258\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CP258\_3 protein").

The nucleotide sequence of CP258\_3 as presently determined is reported in SEQ ID NO:171, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CP258\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:172. Amino acids 3 to 15 of SEQ ID NO:172 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CP258\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CP258\_3 should be approximately 560 bp.

5       The nucleotide sequence disclosed herein for CP258\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

CP258\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 26 kDa was detected in conditioned medium and membrane fractions using  
10   SDS polyacrylamide gel electrophoresis.

#### Clone "CW1155\_3"

A polynucleotide of the present invention has been identified as clone "CW1155\_3". CW1155\_3 was isolated from a human fetal brain cDNA library using methods which are  
15   selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW1155\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW1155\_3 protein").

The nucleotide sequence of CW1155\_3 as presently determined is reported in SEQ ID  
20   NO:173, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW1155\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:174. Amino acids 220 to 232 of SEQ ID NO:174 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 233. Due to the hydrophobic nature of the predicted leader/signal  
25   sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CW1155\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW1155\_3 should be approximately 1170 bp.

The nucleotide sequence disclosed herein for CW1155\_3 was searched against the  
30   GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CW1155\_3 demonstrated at least some similarity with sequences identified as AA169043 (ms36h08.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 613695 5'), D86145 (Rat mRNA), and H29261 (ym32b03.s1 Homo sapiens cDNA clone 49733 3'). Based upon sequence similarity, CW1155\_3 proteins and each similar protein or peptide may share at  
35   least some activity.

Clone "CZ247\_2"

A polynucleotide of the present invention has been identified as clone "CZ247\_2". CZ247\_2 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CZ247\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CZ247\_2 protein").

The nucleotide sequence of CZ247\_2 as presently determined is reported in SEQ ID NO:175, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
10 frame and the predicted amino acid sequence of the CZ247\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:176. Amino acids 545 to 557 of SEQ ID NO:176 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 558. Due to the hydrophobic nature of the predicted leader/signal  
15 sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CZ247\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CZ247\_2 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for CZ247\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
20 protocols. CZ247\_2 demonstrated at least some similarity with sequences identified as T09256 (Human ara Kb beta-galactosidase fusion protein coding sequence), W27222 (26h9 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA), and W72736 (zd71e02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346106 3'). The predicted amino acid sequence disclosed herein for CZ247\_2 was searched against the GenPept and GeneSeq amino acid  
25 sequence databases using the BLASTX search protocol. The predicted CZ247\_2 protein demonstrated at least some similarity to sequences identified as R88069 (Human ara Kb beta-galactosidase fusion protein). Based upon sequence similarity, CZ247\_2 proteins and each similar protein or peptide may share at least some activity.

Clone "AM666\_1"

A polynucleotide of the present invention has been identified as clone "AM666\_1". AM666\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

acid sequence of the encoded protein. AM666\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AM666\_1 protein").

The nucleotide sequence of AM666\_1 as presently determined is reported in SEQ ID NO:177, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
5 frame and the predicted amino acid sequence of the AM666\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:178. Amino acids 15 to 27 of SEQ ID NO:178 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal  
10 sequence not be separated from the remainder of the AM666\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AM666\_1 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for AM666\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA  
15 search protocols. AM666\_1 demonstrated at least some similarity with sequences identified as AA493985 (nh07g08.s1 NCI\_CGAP\_Thy1 Homo sapiens cDNA clone). Based upon sequence similarity, AM666\_1 proteins and each similar protein or peptide may share at least some activity.

AM666\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 17 kDa was detected in membrane fractions using SDS polyacrylamide gel  
20 electrophoresis.

#### Clone "BN387\_3"

A polynucleotide of the present invention has been identified as clone "BN387\_3". BN387\_3 was isolated from a human adult placenta cDNA library using methods which are  
25 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BN387\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BN387\_3 protein").

The nucleotide sequence of BN387\_3 as presently determined is reported in SEQ ID  
30 NO:179, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BN387\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:180. Amino acids 14 to 26 of SEQ ID NO:180 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BN387\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BN387\_3 should be approximately 2000 bp.

5       The nucleotide sequence disclosed herein for BN387\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BN387\_3 demonstrated at least some similarity with sequences identified as H16912 (ym39d01.r1 Homo sapiens cDNA clone 50771 5'). Based upon sequence similarity, BN387\_3 proteins and each similar protein or peptide may share at least some activity.

10       BN387\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 30 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "BQ135\_2"

15       A polynucleotide of the present invention has been identified as clone "BQ135\_2". BQ135\_2 was isolated from a human adult colon (adenocarcinoma Caco2) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BQ135\_2 is a full-length clone,  
20       including the entire coding sequence of a secreted protein (also referred to herein as "BQ135\_2 protein").

      The nucleotide sequence of BQ135\_2 as presently determined is reported in SEQ ID NO:181, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BQ135\_2 protein corresponding to the  
25       foregoing nucleotide sequence is reported in SEQ ID NO:182.

      The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BQ135\_2 should be approximately 1200 bp.

      The nucleotide sequence disclosed herein for BQ135\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
30       protocols. BQ135\_2 demonstrated at least some similarity with sequences identified as AA023751 (mh81f01.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone 457369 5'), AA105433 (ml83g01.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone 518640 5'), D64061 (Rat brain mRNA for annexin V-binding protein (ABP-7), partial cds), and N67257 (yz49b08.s1 Homo sapiens cDNA clone 286359 3'). The predicted amino acid  
35       sequence disclosed herein for BQ135\_2 was searched against the GenPept and GeneSeq amino



acid sequence databases using the BLASTX search protocol. The predicted BQ135\_2 protein demonstrated at least some similarity to sequences identified as D64061 (annexin V-binding protein (ABP-7) [Rattus norvegicus]). Annexins associate with membranes and act as ion channels, they can also act as an autocrine factor that enhances osteoclast formation and bone resorption. Annexins have been localized in nucleoli and mitochondria but also in the cytoplasm, plasma (i.e. blood) and in association with vesicles. They are probably involved in fusing vesicles to each other and to plasma membranes causing secretion of vesicular contents. Specifically they have a calcium-dependent ability to bind phospholipids. Thus they are membrane associated. It is possible that annexin-binding proteins are also membrane associated even though they are highly hydrophilic through the same mechanism (electrostatic interaction with phospholipids of membranes). Based upon sequence similarity, BQ135\_2 proteins and each similar protein or peptide may share at least some activity.

#### Clone "CR678\_1"

A polynucleotide of the present invention has been identified as clone "CR678\_1". CR678\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CR678\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CR678\_1 protein").

The nucleotide sequence of CR678\_1 as presently determined is reported in SEQ ID NO:183, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CR678\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:184.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CR678\_1 should be approximately 870 bp.

The nucleotide sequence disclosed herein for CR678\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CR678\_1 demonstrated at least some similarity with sequences identified as X85232 (H.sapiens chromosome 3 sequences). Based upon sequence similarity, CR678\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CR678\_1 indicates that it may contain an Alu repetitive element.

#### Clone "CW420\_2"

A polynucleotide of the present invention has been identified as clone "CW420\_2". CW420\_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW420\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW420\_2 protein").

The nucleotide sequence of CW420\_2 as presently determined is reported in SEQ ID NO:185, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW420\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:186.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW420\_2 should be approximately 5100 bp.

The nucleotide sequence disclosed herein for CW420\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CW420\_2 demonstrated at least some similarity with sequences identified as T55440 (yb38e09.s1 Homo sapiens cDNA clone 73480 3'). Based upon sequence similarity, CW420\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the CW420\_2 protein sequence centered around amino acids 500 and 1270 of SEQ ID NO:186, respectively.

#### Clone "CW795\_2"

A polynucleotide of the present invention has been identified as clone "CW795\_2". CW795\_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW795\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW795\_2 protein").

The nucleotide sequence of CW795\_2 as presently determined is reported in SEQ ID NO:187, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW795\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:188.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW795\_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for CW795\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA

-330-

search protocols. CW795\_2 demonstrated at least some similarity with sequences identified as AA115676 (zl86a09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511480 3'), N22955 (yw44h07.s1 Homo sapiens cDNA clone 255133 3'), and W56804 (zd16g06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 340858 3'). The predicted amino acid sequence disclosed herein for CW795\_2 was searched against the GenPept, GeneSeq, and SwissProt amino acid sequence databases using the BLASTX search protocol. The predicted CW795\_2 protein demonstrated at least some similarity to sequences identified as X81068 (probable mitochondrial protein) and the yeast proteins rca1 and afg3 (tat-binding homologues). Based upon sequence similarity, CW795\_2 proteins and each similar protein or peptide may share at least some activity.

10 The TopPredII computer program predicts two potential transmembrane domains within the CW795\_2 protein sequence centered around amino acids 60 and 170 of SEQ ID NO:188, respectively.

CW795\_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 10 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15

#### Clone "CW823\_3"

A polynucleotide of the present invention has been identified as clone "CW823\_3". CW823\_3 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW823\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW823\_3 protein").

20

The nucleotide sequence of CW823\_3 as presently determined is reported in SEQ ID NO:189, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW823\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:190.

25

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW823\_3 should be approximately 600 bp.

30 The nucleotide sequence disclosed herein for CW823\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "DF989\_3"

A polynucleotide of the present invention has been identified as clone "DF989\_3". DF989\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DF989\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DF989\_3 protein").

The nucleotide sequence of the 5' portion of DF989\_3 as presently determined is reported in SEQ ID NO:191. What applicants presently believe is the proper reading frame for the coding  
10 region is indicated in SEQ ID NO:192. The predicted amino acid sequence of the DF989\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:192. Amino acids 2 to 14 of SEQ ID NO:192 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the  
15 predicted leader/signal sequence not be separated from the remainder of the DF989\_3 protein. Additional nucleotide sequence from the 3' portion of DF989\_3, including a poly(A) tail, is reported in SEQ ID NO:193.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DF989\_3 should be approximately 1800 bp.

20 The nucleotide sequence disclosed herein for DF989\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. DF989\_3 demonstrated at least some similarity with sequences identified as R24724 (yg43c05.r1 Homo sapiens cDNA clone 35337 5') and T33717 (EST58870 Homo sapiens cDNA 5' end similar to None). Based upon sequence similarity, DF989\_3 proteins and each similar  
25 protein or peptide may share at least some activity.

Clone "DL162\_1"

A polynucleotide of the present invention has been identified as clone "DL162\_1". DL162\_1 was isolated from a human adult brain cDNA library using methods which are selective  
30 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DL162\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DL162\_1 protein").

The nucleotide sequence of DL162\_1 as presently determined is reported in SEQ ID  
35 NO:194, and includes a poly(A) tail. What applicants presently believe to be the proper reading

frame and the predicted amino acid sequence of the DL162\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:195. Amino acids 28 to 40 of SEQ ID NO:195 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the DL162\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DL162\_1 should be approximately 875 bp.

The nucleotide sequence disclosed herein for DL162\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

#### Clone "DL162\_2"

A polynucleotide of the present invention has been identified as clone "DL162\_2". DL162\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DL162\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DL162\_2 protein").

The nucleotide sequence of DL162\_2 as presently determined is reported in SEQ ID NO:196, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the DL162\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:197. Amino acids 1 to 13 of SEQ ID NO:197 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 14. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the DL162\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DL162\_2 should be approximately 4000 bp.

The predicted amino acid sequence disclosed herein for DL162\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted DL162\_2 protein demonstrated at least some similarity to sequences identified as AB002309 (KIAA0311 protein [Homo sapiens]). The TopPredII computer program predicts a potential transmembrane domains within the DL162\_2 protein sequence near the carboxyl terminus of SEQ ID NO:197.

DL162\_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 160 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5        Clone "EC172\_1"

A polynucleotide of the present invention has been identified as clone "EC172\_1". EC172\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. EC172\_1 is a full-length clone, including the entire coding sequence of  
10        a secreted protein (also referred to herein as "EC172\_1 protein").

The nucleotide sequence of EC172\_1 as presently determined is reported in SEQ ID NO:198, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the EC172\_1 protein corresponding to the  
15        foregoing nucleotide sequence is reported in SEQ ID NO:199. Amino acids 659 to 671 of SEQ ID NO:199 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 672. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the EC172\_1 protein.

20        The EcoRI/NotI restriction fragment obtainable from the deposit containing clone EC172\_1 should be approximately 4000 bp.

The nucleotide sequence disclosed herein for EC172\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. EC172\_1 demonstrated at least some similarity with sequences identified as H31192  
25        (EST104991 Rattus sp. cDNA 3' end similar to C.elegans hypothetical protein ZK1098.10) and U29585 (Streptococcus pyogenes emm18.1). The predicted amino acid sequence disclosed herein for EC172\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted EC172\_1 protein demonstrated at least some similarity to sequences identified as Z22176 (ZK1098.10 [Caenorhabditis elegans]). Based upon  
30        sequence similarity, EC172\_1 proteins and each similar protein or peptide may share at least some activity.

Deposit of Clones

Clones AX65\_22, BD335\_14, BG241\_1, BL187\_4, BL249\_18, BO71\_1, BO365\_2,  
35        BV51\_1, BV140\_3, BV141\_2, CC194\_4, and DA136\_11 were deposited on October 3, 1996 with

the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98196, from which each clone comprising a particular polynucleotide is obtainable.

5 Clones AR415\_4, AS63\_29, BG160\_1, BO432\_4, BO538\_2, BR595\_4, CI490\_2, CI522\_1, CN238\_1, CO390\_1, and AY304\_1 (an additional isolate of clone AY304\_14) were deposited on October 25, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98232, from which each clone comprising  
10 a particular polynucleotide is obtainable. Clone AY304\_14 was deposited on October 23, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98561.

Clones AJ20\_2, AR440\_1, AS164\_1, AX8\_1, BD176\_3, BD339\_1, BD427\_1, BL229\_22,  
15 BV123\_16, and CH377\_1 were deposited on November 15, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98261, from which each clone comprising a particular polynucleotide is obtainable.

Clones BD441\_1, BD441\_2, BG102\_3, BK158\_1, BP163\_1, BZ16\_3, CC182\_1,  
20 CG109\_1 and CJ397\_1 were deposited on November 20, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98264, from which each clone comprising a particular polynucleotide is obtainable.

Clones AM795\_4, AT340\_1, BG132\_1, BG219\_2, BG366\_2, BV172\_2, CC247\_10,  
25 CI480\_9, CO722\_1, and CT748\_2 were deposited on December 5, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98271, from which each clone comprising a particular polynucleotide is obtainable.

Clones AJ1\_1, AQ73\_3, BG142\_1, BV66\_1, BV291\_3, CK201\_1, CQ331\_2, CT550\_1,  
30 CT585\_1 and CT797\_3 were deposited on December 13, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98278, from which each clone comprising a particular polynucleotide is obtainable.

Clones CB107\_1, CG300\_3, CJ145\_1, CJ160\_11, CO20\_1, CO223\_1, CO310\_2,  
35 CP258\_3, CW1155\_3 and CZ247\_2 were deposited on December 17, 1996 with the ATCC

(American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98279, from which each clone comprising a particular polynucleotide is obtainable. Clone CO223\_3 was deposited on January 9, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98291.

Clones AM666\_1, BN387\_3, BQ135\_2, CR678\_1, CW420\_2, CW795\_2, CW823\_3, DF989\_3, DL162\_2, DL162\_1, and EC172\_1 were deposited on January 10, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98292, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in this composite deposit. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.



	<u>Clone</u>	<u>Probe Sequence</u>
	AX65_22	SEQ ID NO:200
	BD335_14	SEQ ID NO:201
	BG241_1	SEQ ID NO:202
5	BL187_4	SEQ ID NO:203
	BL249_18	SEQ ID NO:204
	BO71_1	SEQ ID NO:205
	BO365_2	SEQ ID NO:206
	BV51_1	SEQ ID NO:207
10	BV140_3	SEQ ID NO:208
	BV141_2	SEQ ID NO:209
	CC194_4	SEQ ID NO:210
	DA136_11	SEQ ID NO:211
	AR415_4	SEQ ID NO:212
15	AS63_29	SEQ ID NO:213
	AY304_14	SEQ ID NO:214
	BG160_1	SEQ ID NO:215
	BO432_4	SEQ ID NO:216
	BO538_2	SEQ ID NO:217
20	BR595_4	SEQ ID NO:218
	CI490_2	SEQ ID NO:219
	CI522_1	SEQ ID NO:220
	CN238_1	SEQ ID NO:221
	CO390_1	SEQ ID NO:222
25	AJ20_2	SEQ ID NO:223
	AR440_1	SEQ ID NO:224
	AS164_1	SEQ ID NO:225
	AX8_1	SEQ ID NO:226
	BD176_3	SEQ ID NO:227
30	BD339_1	SEQ ID NO:228
	BD427_1	SEQ ID NO:229
	BL229_22	SEQ ID NO:230
	BV123_16	SEQ ID NO:231
	CH377_1	SEQ ID NO:232
35	BD441_1	SEQ ID NO:233

	BD441_2	SEQ ID NO:234
	BG102_3	SEQ ID NO:235
	BK158_1	SEQ ID NO:236
	BP163_1	SEQ ID NO:237
5	BZ16_3	SEQ ID NO:238
	CC182_1	SEQ ID NO:239
	CG109_1	SEQ ID NO:240
	CJ397_1	SEQ ID NO:241
	AM795_4	SEQ ID NO:242
10	AT340_1	SEQ ID NO:243
	BG132_1	SEQ ID NO:244
	BG219_2	SEQ ID NO:245
	BG366_2	SEQ ID NO:246
	BV172_2	SEQ ID NO:247
15	CC247_10	SEQ ID NO:248
	CI480_9	SEQ ID NO:249
	CO722_1	SEQ ID NO:250
	CT748_2	SEQ ID NO:251
	AJ1_1	SEQ ID NO:252
20	AQ73_3	SEQ ID NO:253
	BG142_1	SEQ ID NO:254
	BV66_1	SEQ ID NO:255
	BV291_3	SEQ ID NO:256
	CK201_1	SEQ ID NO:257
25	CQ331_2	SEQ ID NO:258
	CT550_1	SEQ ID NO:259
	CT585_1	SEQ ID NO:260, SEQ ID NO:262
	CT797_3	SEQ ID NO:261
	CB107_1	SEQ ID NO:263
30	CG300_3	SEQ ID NO:264
	CJ145_1	SEQ ID NO:265
	CJ160_11	SEQ ID NO:266
	CO20_1	SEQ ID NO:267
	CO223_3	SEQ ID NO:268
35	CO310_2	SEQ ID NO:269

	CP258_3	SEQ ID NO:270
	CW1155_3	SEQ ID NO:271
	CZ247_2	SEQ ID NO:272
	AM666_1	SEQ ID NO:273
5	BN387_3	SEQ ID NO:274
	BQ135_2	SEQ ID NO:275
	CR678_1	SEQ ID NO:276
	CW420_2	SEQ ID NO:277
	CW795_2	SEQ ID NO:278
10	CW823_3	SEQ ID NO:279
	DF989_3	SEQ ID NO:280
	DL162_1, DL162_2	SEQ ID NO:281
	EC172_1	SEQ ID NO:282

15 In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

20 The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b) It should be designed to have a  $T_m$  of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

25 The oligonucleotide should preferably be labeled with  $\gamma$ -<sup>32</sup>P ATP (specific activity 6000 Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a

30 scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmol.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100  $\mu$ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100  $\mu$ g/ml. The culture should preferably be grown to saturation at 37°C,

35 and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions

should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 µg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein

may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with the ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

5           The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' 10 untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" 15 is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

          The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the 20 corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession 25 number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

30           Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and 35 Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by

reference herein). The desired change in gene expression can also be achieved through the use of double-stranded ribonucleotide molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA interference" or "RNAi"; Fire *et al.*, 1998, *Nature* 391 (6669): 806-811; 5 Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* 95 (26): 15502-15507; and Sharp, 1999, *Genes Dev.* 13 (2): 139-141; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic 10 animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the 15 corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through 20 homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models 25 for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the 30 intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains

which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* 266: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* 215: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins

and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).



The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity  
5 (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic  
10 acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent  
15 conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer <sup>†</sup>	Wash Temperature and Buffer <sup>†</sup>
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	<50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
10	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T <sub>J</sub> *; 4xSSC	T <sub>J</sub> *; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	<50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

<sup>‡</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>†</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory*

*Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

5 Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

10 The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

20 A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

25 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include 30 *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the  
5 MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under  
10 culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-  
15 toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of  
20 maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available  
25 from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially  
30 homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized  
35 by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

#### USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

#### Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding

protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential  
5 genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as  
10 an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi  
15 *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in  
20 assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can  
25 be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

30 Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate.

- 5 In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

10

### Cytokine and Cell Proliferation/Differentiation Activity

- A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK. The activity of a protein of the invention may, among other means, be measured by the following methods:

- Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

- Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: *Polyclonal T cell stimulation*, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and *Measurement of mouse and human Interferon  $\gamma$* , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; 5 deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, 10 S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins 15 that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic 20 studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

25 A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells 30 and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as



candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, 5 rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression 10 is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The 15 functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists 20 after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level 25 lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule 30 which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the 35 corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter

prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral

diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed  
5 APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and  
10 reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a  
15 nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like  
20 activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells  
25 to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC  
30 class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant  
35 chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B

lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

5 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic  
10 studies in Humans); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.*  
15 137:3494-3500, 1986; Bowman et al., *J. Virology* 61:1992-1998; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect  
20 Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins  
25 that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512,  
30 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et  
35 al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology*

67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5        Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and*  
10 *Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al.,  
15 *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21,  
20 Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

25

#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

30        A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an

osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming  
5 cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

10 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a  
15 tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also  
20 useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention  
25 may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral  
30 nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral  
35 sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with

the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of



inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation,

those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 5 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a  
10 result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of  
15 cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res.  
20 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor  
25 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen  
30 recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160, 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

10

#### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions, including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

25

#### Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The

35

cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

5 E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

30 Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity,

preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

#### Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an

immune response against such protein or another material or entity which is cross-reactive with such protein.

#### **ADMINISTRATION AND DOSING**

5           A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable"

10 means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2,

15 G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in

20 formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or

25 homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will

30 respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with

35 co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind

surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in  
5 which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such  
10 liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a  
15 meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination,  
20 serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments  
25 employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering  
30 protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous,

intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g



to about 100 mg (preferably about 0.1 mg to about 10 mg, more preferably about 0.1  $\mu$ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein. Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for

example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite,

polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, 5 or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid 10 in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, 15 hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total 20 formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents 25 beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. 30 Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the 35 site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue

(e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final  
5 composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a  
10 mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can  
15 then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - (a) the nucleotide sequence of SEQ ID NO:41;
  - (b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027;
  - (c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027;
  - (d) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431;
  - (e) the nucleotide sequence of the full-length protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232;
  - (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;
  - (g) the nucleotide sequence of a mature protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232;
  - (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;
  - (i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
  - (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
  - (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
  - (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:41.
2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.

4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
  - (a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and
  - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. An isolated polynucleotide encoding the protein of claim 6.
8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232.
9. A protein comprising an amino acid sequence selected from the group consisting of:
  - (a) the amino acid sequence of SEQ ID NO:42;
  - (b) the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;the protein being substantially free from other mammalian proteins.
10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:42.
11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.
12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - (a) the nucleotide sequence of SEQ ID NO:129;

- (b) the nucleotide sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958;
- (c) the nucleotide sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958;
- (d) the nucleotide sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488;
- (e) the nucleotide sequence of the full-length protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (g) the nucleotide sequence of a mature protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:130;
- (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
- (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:129.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:130;
- (b) the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34;
- (c) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and

(d) the amino acid sequence encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271; the protein being substantially free from other mammalian proteins.



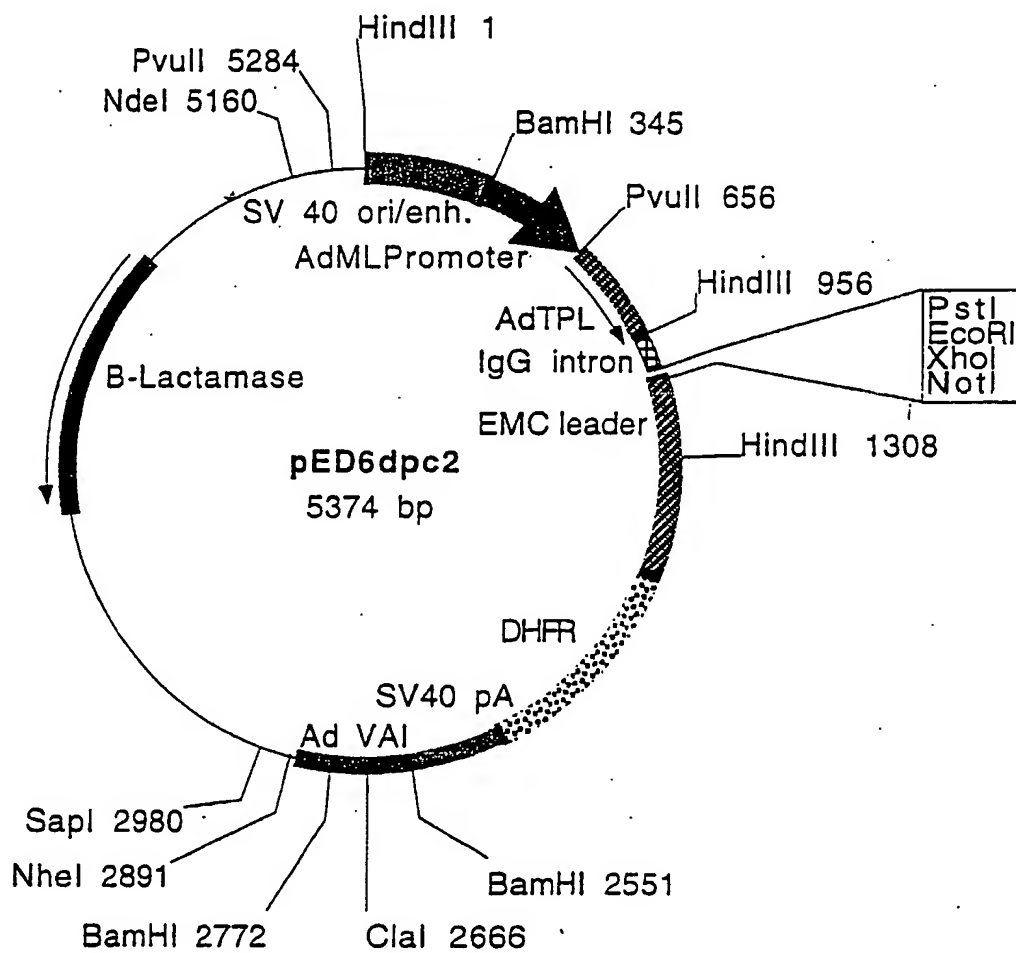


Fig. 1A

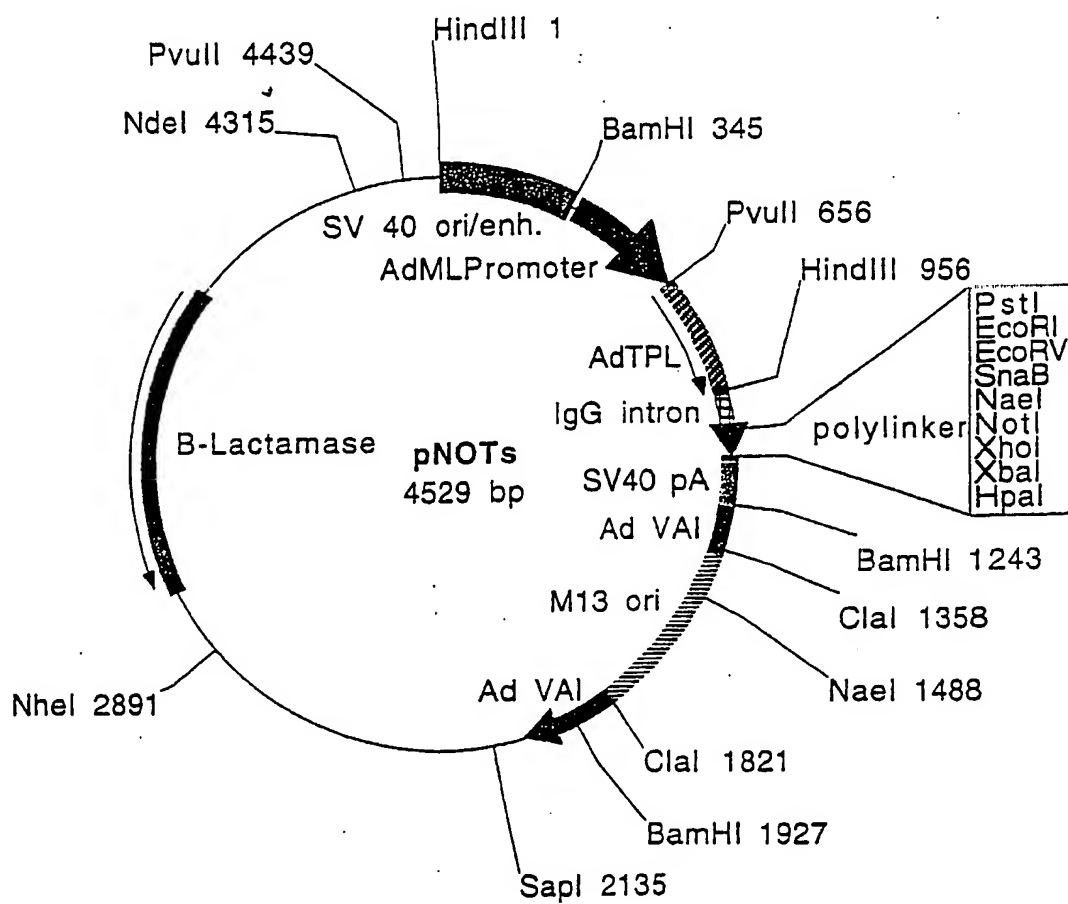


Fig. 1B

## SEQUENCE LISTING

<110> Jacobs, Kenneth  
McCoy, John M.  
LaVallie, Edward R.  
Collins-Racie, Lisa A.  
Evans, Cheryl  
Merberg, David  
Treacy, Maurice  
Bowman, Michael R.  
Spaulding, Vikki  
Agostino, Michael J.  
Genetics Institute, Inc.

<120> SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

<130> GI 6011-18X

<140>  
<141>

<160> 283

<170> PatentIn Ver. 2.0

<210> 1  
<211> 565  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (20)

<220>  
<221> unsure  
<222> (49)

<220>  
<221> unsure  
<222> (58)

<220>  
<221> unsure  
<222> (144)

<220>  
<221> unsure  
<222> (178)

<220>  
<221> unsure  
<222> (215)

<220>  
<221> unsure  
<222> (218)

<220>  
<221> unsure

&lt;222&gt; (228)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (239)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (541)

&lt;400&gt; 1

```

gattgtcagt ttccaaaaan gaggaggatt tgatattcac ttggcccgng gtgatgcntt 60
tgaggggtggc cgcgtccatc tggtcagaaa agacaatctt ttgtttgtca agcttgaggt 120
gtggcaggct tgagatctgg ccanacactt gaggagacaat gacatccact ttgctttntc 180
tccacagggtg tccactccca ggtccaactg caganttnga attcggcntt catggcctnt 240
gaatagagac ttctggactc tatagaaccc actgcctcct gatgaagtcc ctactgttca 300
cccttgccagt ttttatgctc ctggcccaat tggcttcagg taattggtat gtgaaaaagt 360
gtctaaacga cgttggaatt tgcaagaaga agtgcaaaccc tgaagagatg cataaaaaaga 420
ctacaagaat ttcaacagta acagcaacaa cagtcaacaa caactttgat gatgactact 480
gcttcgatgt cttcgatggc tctacccgt ttctccact ggtggaacat tcccagcctc 540
ngtctcctgc tctaggatcc ccgac 565

```

&lt;210&gt; 2

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (87)

&lt;400&gt; 2

```

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
  1             5             10             15

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
      20             25             30

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Thr Lys Thr Thr
      35             40             45

Arg Ile Ser Thr Val Thr Ala Thr Thr Val Asn Asn Asn Phe Asp Asp
      50             55             60

Asp Tyr Cys Phe Asp Val Phe Asp Gly Ser Tyr Pro Phe Leu Pro Leu
      65             70             75             80

Val Glu His Ser Gln Pro Xaa Ser Pro Ala Leu Gly Ser Pro
      85             90

```

&lt;210&gt; 3

&lt;211&gt; 92

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

```

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 92

```

&lt;210&gt; 4

&lt;211&gt; 2949

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

acctgctgga acgctcggac gtccttgccg gccctgtcca tgtgaggtcc aggtcatctc 60  
ccgccaccgc agacaagcgc caggatgtgc ttttggggca agacagtggc tttggtcttg 120  
tgaaggatcc atgttatattg gctggtcctg gatctaggtc actcagttgt tcagaaagag 180  
gccaagaaga gatgctgccg ctcttccacc atctcaccgc tcgttggggg ggttcaggct 240  
gcaaagccat tgggtgattcc tccgttccta gtgaatgtcc tggaaacctg gaccatcaga 300  
ggcaagccag taggacaccc tggcccaggc caccactggc aggaacgcaa gggctggcca 360  
cagacaccag ggctgcaccc ctgaccccaa ttggcaccgc tctgccttca gccattccct 420  
ctggctactg ctacaggac ggtcagacag ggcgacagcc tctcccgccc tacacccttg 480  
ccatgatgca cagaagcaat ggtcacaccc tgaccagcc tcccgggtcca agaggctgtg 540  
agggcgatgg cccagagcat ggggtagaag agggaaacgag gaagagggtc tcgctgcctc 600  
agtggccacc tcttctctga gcaaagtggg cccacgcagc cagagaggac agccttccctg 660  
aggaatcctc agccccctgat tttgcaaac tgaaagcacta tcaaaaacag cagagtcttc 720  
caagtttatg cagcacttct gaccagaca cactctcttg ggcctccgagc actccaggga 780  
ggatctccct ccgaatatct gagtctgtcc tgcgggactc cccgccacct catgaggatt 840  
atgaagacga agtgtttgtg agggatccgc accccaaggc cactgtccagc cccacatttg 900  
aacctctctc cccacccccca cctctctcac cgagtcagga aacccccggtg tatakcatgg 960  
atgacttccc tccacctcct cccacactg tatgtgaggc gcagctggac agtgaggatc 1020  
ccgagggggc acgccccagc ttcaacaaac tttctaaagt gacaattgca agggaaaggc 1080  
acatgcctgg tgcagcccat gtggtaggta gtcagacact ggcttccaga ctccaaactt 1140  
ctatcaaggg ttcagaggct gagtccacac caccctcctt catgagcgtt cagcccaac 1200  
ttgctgggtc tcttgggtgg cagccagcac ccatccagac tcaaaacctc agccatgatc 1260  
cagtcagtgg aactcagggt ttagaaaaga aagtcagtc tgatcctcag aagagttcag 1320  
aagacatcag aacagaggct ttggccaagg aaattgtcca ccaagacaaa tctctagcag 1380  
acattttgga tccagactcc aggctgaaga caacaatgga cctgatggaa ggtttgtttc 1440  
cccagatagt gaacttgctg aaggaaaaca gtgtaaagag gaaggccata cagagaactg 1500  
tcagctcttc aggatgtgaa ggcaagagga atgaagacaa ggaagcagtg agcatgttg 1560  
ttaactgccc tgcctactac agtgtgtctg ctcccaaggc tgagctactg aacaaaatca 1620  
aagagatgcc acgagaagtg aatgaggaag aggaacaggc agatgtcaat gaaaagaagg 1680  
ctgagctcat tggaaagtcc acccacaagc tggagaccct ccaggaggcg aaggggagcc 1740  
tgctcacgga catcaagctc aacaacgccc tgggagaaga ggtggaggct ctgacagcg 1800  
agctctgcaa gcccaatgag tttgacaagt ataggatgt cataggggat ttggacaagg 1860  
tggtaacctt gctgctctcc ctctcggggc gtctagcccg tgttgagaat gtccttagcg 1920  
gccttgggtc agatggcagt aatgaagaaa ggagctctct ttacgagaaa aggaagatcc 1980  
tggctgggtc gcatgaggat gccccggagc tgaaggagaa cctggatcgc agggagcgag 2040  
tagtgcctgg catcttggcc aattaccttt cagaggagca gctccaggac taccagcact 2100  
tcgtgaaaaa gaagtccacg ctctctattg agcaacggaa gctggatgac aagatcaagc 2160  
tggggccagg gcaaggtcaag tgtctgctgg agagcctgcc ctccagatttc attcccaagg 2220  
ctggggccct ggctctgccc ccaaacctca cgagttagcc cattcctgct gggggctgta 2280  
ctttcagtggt tattttccca acattaacct ctccacttta acctcttcta aaatacccaa 2340  
ccaaaagatc actgtttctc tcaacactat ttaattctga aaatgtttca gtacaaacca 2400  
ctgtttgaac tatctgggtt attgggtgtt gttcctgatg aaaggaaaaa aattctctcc 2460  
aggagggaagc ctttttccct cttgcccctc ctgattgatc ttctgagagc tcgaatgtcg 2520  
ctggacacgt accccttcta ttattacttt gtagtagaaa gaaagttaat gaaactgaga 2580  
actgattgga ggggtgtttg tcatttagtt ttaaacaggc tgaggcaaca tggatcagtg 2640  
tgtgtccccc tcaggaatgt atccacagtg gccttccttg ctgggtgggca gtgtatcctg 2700  
atggcagggt acaagtacca ttaatgaagg gtctgcaaca taaagcctta aaaagacaca 2760  
cactaagaaa actgtaaaac cttgaacatt gttatttata ttttttaaaa tggaaaagat 2820  
cactatgttt gttgtgctaa ccacttattt gattctgttt tgtgggtggac atagatgatt 2880  
acgttttagc tttgtatttt gtgaaaacct taatgaaatg aattccaaag ataaaaaaaa 2940  
aaaaaaaaa 2949

&lt;210&gt; 5

&lt;211&gt; 709

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (255)

&lt;400&gt; 5

Met Leu Pro Leu Phe His His Leu Thr Pro Arg Trp Gly Gly Ser Gly  
 1 5 10 15

Cys Lys Ala Ile Gly Asp Ser Ser Val Pro Ser Glu Cys Pro Gly Thr  
 20 25 30

Leu Asp His Gln Arg Gln Ala Ser Arg Thr Pro Cys Pro Arg Pro Pro  
 35 40 45

Leu Ala Gly Thr Gln Gly Leu Val Thr Asp Thr Arg Ala Ala Pro Leu  
 50 55 60

Thr Pro Ile Gly Thr Pro Leu Pro Ser Ala Ile Pro Ser Gly Tyr Cys  
 65 70 75 80

Ser Gln Asp Gly Gln Thr Gly Arg Gln Pro Leu Pro Pro Tyr Thr Pro  
 85 90 95

Ala Met Met His Arg Ser Asn Gly His Thr Leu Thr Gln Pro Pro Gly  
 100 105 110

Pro Arg Gly Cys Glu Gly Asp Gly Pro Glu His Gly Val Glu Glu Gly  
 115 120 125

Thr Arg Lys Arg Val Ser Leu Pro Gln Trp Pro Pro Pro Ser Arg Ala  
 130 135 140

Lys Trp Ala His Ala Ala Arg Glu Asp Ser Leu Pro Glu Glu Ser Ser  
 145 150 155 160

Ala Pro Asp Phe Ala Asn Leu Lys His Tyr Gln Lys Gln Gln Ser Leu  
 165 170 175

Pro Ser Leu Cys Ser Thr Ser Asp Pro Asp Thr Pro Leu Gly Ala Pro  
 180 185 190

Ser Thr Pro Gly Arg Ile Ser Leu Arg Ile Ser Glu Ser Val Leu Arg  
 195 200 205

Asp Ser Pro Pro Pro His Glu Asp Tyr Glu Asp Glu Val Phe Val Arg  
 210 215 220

Asp Pro His Pro Lys Ala Thr Ser Ser Pro Thr Phe Glu Pro Leu Pro  
 225 230 235 240

Pro Pro Pro Pro Pro Pro Ser Gln Glu Thr Pro Val Tyr Xaa Met  
 245 250 255

Asp Asp Phe Pro Pro Pro Pro Pro His Thr Val Cys Glu Ala Gln Leu  
 260 265 270

Asp Ser Glu Asp Pro Glu Gly Pro Arg Pro Ser Phe Asn Lys Leu Ser  
 275 280 285

Lys Val Thr Ile Ala Arg Glu Arg His Met Pro Gly Ala Ala His Val  
 290 295 300  
 Val Gly Ser Gln Thr Leu Ala Ser Arg Leu Gln Thr Ser Ile Lys Gly  
 305 310 315 320  
 Ser Glu Ala Glu Ser Thr Pro Pro Ser Phe Met Ser Val His Ala Gln  
 325 330 335  
 Leu Ala Gly Ser Leu Gly Gly Gln Pro Ala Pro Ile Gln Thr Gln Ser  
 340 345 350  
 Leu Ser His Asp Pro Val Ser Gly Thr Gln Gly Leu Glu Lys Lys Val  
 355 360 365  
 Ser Pro Asp Pro Gln Lys Ser Ser Glu Asp Ile Arg Thr Glu Ala Leu  
 370 375 380  
 Ala Lys Glu Ile Val His Gln Asp Lys Ser Leu Ala Asp Ile Leu Asp  
 385 390 395 400  
 Pro Asp Ser Arg Leu Lys Thr Thr Met Asp Leu Met Glu Gly Leu Phe  
 405 410 415  
 Pro Arg Asp Val Asn Leu Leu Lys Glu Asn Ser Val Lys Arg Lys Ala  
 420 425 430  
 Ile Gln Arg Thr Val Ser Ser Ser Gly Cys Glu Gly Lys Arg Asn Glu  
 435 440 445  
 Asp Lys Glu Ala Val Ser Met Leu Val Asn Cys Pro Ala Tyr Tyr Ser  
 450 455 460  
 Val Ser Ala Pro Lys Ala Glu Leu Leu Asn Lys Ile Lys Glu Met Pro  
 465 470 475 480  
 Ala Glu Val Asn Glu Glu Glu Gln Ala Asp Val Asn Glu Lys Lys  
 485 490 495  
 Ala Glu Leu Ile Gly Ser Leu Thr His Lys Leu Glu Thr Leu Gln Glu  
 500 505 510  
 Ala Lys Gly Ser Leu Leu Thr Asp Ile Lys Leu Asn Asn Ala Leu Gly  
 515 520 525  
 Glu Glu Val Glu Ala Leu Ile Ser Glu Leu Cys Lys Pro Asn Glu Phe  
 530 535 540  
 Asp Lys Tyr Arg Met Phe Ile Gly Asp Leu Asp Lys Val Val Asn Leu  
 545 550 555 560  
 Leu Leu Ser Leu Ser Gly Arg Leu Ala Arg Val Glu Asn Val Leu Ser  
 565 570 575  
 Gly Leu Gly Glu Asp Ala Ser Asn Glu Glu Arg Ser Ser Leu Tyr Glu  
 580 585 590  
 Lys Arg Lys Ile Leu Ala Gly Gln His Glu Asp Ala Arg Glu Leu Lys  
 595 600 605

Glu Asn Leu Asp Arg Arg Glu Arg Val Val Leu Gly Ile Leu Ala Asn  
 610 615 620  
 Tyr Leu Ser Glu Glu Gln Leu Gln Asp Tyr Gln His Phe Val Lys Met  
 625 630 635 640  
 Lys Ser Thr Leu Leu Ile Glu Gln Arg Lys Leu Asp Asp Lys Ile Lys  
 645 650 655  
 Leu Gly Gln Glu Gln Val Lys Cys Leu Leu Glu Ser Leu Pro Ser Asp  
 660 665 670  
 Phe Ile Pro Lys Ala Gly Ala Leu Ala Leu Pro Pro Asn Leu Thr Ser  
 675 680 685  
 Glu Pro Ile Pro Ala Gly Gly Cys Thr Phe Ser Gly Ile Phe Pro Thr  
 690 695 700  
 Leu Thr Ser Pro Leu  
 705

<210> 6  
 <211> 190  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (4)

<220>  
 <221> unsure  
 <222> (30)

<220>  
 <221> unsure  
 <222> (97)

<220>  
 <221> unsure  
 <222> (154)

<220>  
 <221> unsure  
 <222> (174)

<400> 6  
 cgangcgtct gcacccacac gctcacgaan catcaggagc ctgtctatag cgtatctttc 60  
 agccctgatg ggaagtactt ggccagtgga tccttenaca agtgcgtcca tatctggaat 120  
 actcagagtg gaaatcttgt ccacagctac cgangcactg gcggcatctt ccangtgtgc 180  
 tggaacgcgc 190

<210> 7  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 7



gagtggaaaag gcagggggag gggcaggag caacagaagg aagagacaac aagcccaaga 60  
 cagcttccat ttcagacgga aggccccag aagatagaat tccagccgac tgaaaaacca 120  
 cccaatgaac aaagaagatt ttagaaaata gaaagctgtt gggattacaa agttgcgcgt 180  
 ttcacggta caaactggtc tttgaacctc ctttgtgaga gcaattgtag tgtccaaatt 240  
 gttagggaaa acaaaaaaaaa aaaatcccaa ggaggagggt tttccccct tccctgttg 300  
 gtttatcaca gcattttgct tttttttgg cacagctttt tacgtttctt tccattcagc 360  
 catcacagag cctgttccgg gtggaaacca a 391

<210> 8

<211> 62

<212> PRT

<213> Homo sapiens

<400> 8

Thr Ser Phe Val Arg Ala Ile Val Val Ser Lys Leu Leu Gly Lys Thr  
 1 5 10 15

Lys Lys Lys Asn Pro Lys Glu Glu Gly Phe Ser Pro Phe Pro Val Trp  
 20 25 30

Phe Ile Thr Ala Phe Cys Phe Phe Phe Gly Thr Ala Phe Tyr Val Ser  
 35 40 45

Phe His Ser Ala Ile Thr Glu Pro Val Pro Gly Gly Asn Gln  
 50 55 60

<210> 9

<211> 267

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (21)

<400> 9

tctctctctc tctccctctg nacctttctc atagttgctt cagatcttag gtetcaagg 60  
 cactttggcg cgtagtaagt gctttatgta agaaggcagg gcaggggggc tttttacagg 120  
 agaaaaaaaa atgacttata agagaaagag cctggagtat ttttggaaaa aaaaataata 180  
 tttttatggt aaaacaattt taaaatctta aaatggccat cagacataga gagcttttg 240  
 tgattcatgt tttaaaaaaaa aaaaaaa 267

<210> 10

<211> 2178

<212> DNA

<213> Homo sapiens

<400> 10

cttttaacgg tcactcggcc ttaarcgctc ctgggtgtat gtgaggctga aagggaagga 60  
 rgaacagggt ctgggccgct gtgtgctctg ccgtcatctc taaraaacia ccataccact 120  
 gaatgctact gtgtacttac aaaccacact catattcgtc acgtcatttc atcttcaccc 180  
 ccacctccaa atgaggcttg aaatgaagat gaagatgttc ctccctcccc tttcaacat 240  
 ggacctcaca ctgtggactt cctcttagag cctctgagtt aggtacccaa gccaaggcac 300  
 aatgtccctg cccccataa gactgccag cccctatggc tctgatecggc tggtagagct 360  
 agcagccagg ctccggccag cactctgtga tactctgac accgtaggga gccaggagtt 420  
 ccccgccac agcctggtgc tagcaggtgt cagccagcag ctgggccgca ggggccagt 480  
 ggctctggga gaaggcatca gccctctac ctttgccag ctctgaact ttgtgtatgg 540  
 ggagagtgt gagctgcagc ctggagagct aagggccctt caggaggcgg ccagggcctt 600  
 gggagtgcag tccctggaag aggcagctg gagggtcga ggggacagg ctaaaaagcc 660

```

agatccaggc ctgaagaaac atcaggagga gccagagaaa ccctcaagga atcctgagag 720
agaactgggg gaccctggag agaagcagaa accagaacag gtttctagaa ctggtgggag 780
agaacaggag atgttgacac agcactcgcc accaagaggc agacccgaga tggcaggagc 840
aacgcaggag gctcagcagg aacagaccag gtcaaaggag aaacgcctcc aagccccctgt 900
tgcccaaagg ggagcagatg ggaagcatgg agtgctcacg tgggtgaggg aaaatccagg 960
gggctctgag gaaagtctgc gcaagctccc tggcccccct cccccagcag gctccctgca 1020
aaccagcgtc acccctaggc cctcgtgggc tgaggccccct tgggtgggtgg ggggcccagcc 1080
tgccctgtgg agcatcctgc tgatgcggcc cagatatggc attcccttct accatagcac 1140
ccccaccact ggagcctggc aggaggtctg gcgggaacag aggatccac tgtccctaaa 1200
tgcccccata gggctctgga gccagaacca gttggccctc tccagcccta ccccagggtc 1260
cctccccag gggcccgac agctcagccc tggggagatg gaagagtctg atcaggggca 1320
cacaggcgca cttgcaacct gtgcgggtca tgaggacaag gcaggctgcc cacctcgccc 1380
gcacctccc ccggccctc ctgctcggtc tcggccctat gcgtgctctg tctgtggaaa 1440
gaggttttca ctcaagcatc agatggagac gcactaccga gtccacacag gagagaagcc 1500
cttctctgt agcctttgtc ctcagcgctc ccgggacttc tcggccatga ccaagcacct 1560
gcggacacac gggcccgctc cgtaccgctg ctccctgtgc ggggcccggc gtcccgacct 1620
ggcctccatg caggcgacac tgcgcgggtca ctgcgccagc caactcccgc ccggatggac 1680
catccgctcc acctctctct actcctctc gagggcgtct cggccctcga cctctccctg 1740
ttgtccttct tctccacca cctgacgggg tgcgggtagc gtcttagcca agagtccaat 1800
taaagaacga aaagcgggcc ggctcggcct ctgacctggc accgctgcta cggcggccta 1860
gcaaattccg ccccgagaag gcccaggaa gggcgccgag tgccctctcc tggacgateg 1920
cgggtcgcag aagcccaggc cagcgagccc tacagagtga ggacactgaa gtgtgcagga 1980
gcgaaggtta acagtagggg agattgtcga tctcatcacc ataataaaga gtttctctgt 2040
gccctccctt caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2100
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2160
aaaaaaaaaa aaaaaaaaaa 2178

```

<210> 11  
<211> 487  
<212> PRT  
<213> Homo sapiens

<400> 11  
Met Ser Leu Pro Pro Ile Arg Leu Pro Ser Pro Tyr Gly Ser Asp Arg  
1 5 10 15  
Leu Val Gln Leu Ala Ala Arg Leu Arg Pro Ala Leu Cys Asp Thr Leu  
20 25 30  
Ile Thr Val Gly Ser Gln Glu Phe Pro Ala His Ser Leu Val Leu Ala  
35 40 45  
Gly Val Ser Gln Gln Leu Gly Arg Arg Gly Gln Trp Ala Leu Gly Glu  
50 55 60  
Gly Ile Ser Pro Ser Thr Phe Ala Gln Leu Leu Asn Phe Val Tyr Gly  
65 70 75 80  
Glu Ser Val Glu Leu Gln Pro Gly Glu Leu Arg Pro Leu Gln Glu Ala  
85 90 95  
Ala Arg Ala Leu Gly Val Gln Ser Leu Glu Glu Ala Cys Trp Arg Ala  
100 105 110  
Arg Gly Asp Arg Ala Lys Lys Pro Asp Pro Gly Leu Lys Lys His Gln  
115 120 125  
Glu Glu Pro Glu Lys Pro Ser Arg Asn Pro Glu Arg Glu Leu Gly Asp  
130 135 140

Pro Gly Glu Lys Gln Lys Pro Glu Gln Val Ser Arg Thr Gly Gly Arg  
 145 150 155 160  
 Glu Gln Glu Met Leu His Lys His Ser Pro Pro Arg Gly Arg Pro Glu  
 165 170 175  
 Met Ala Gly Ala Thr Gln Glu Ala Gln Gln Glu Gln Thr Arg Ser Lys  
 180 185 190  
 Glu Lys Arg Leu Gln Ala Pro Val Gly Gln Arg Gly Ala Asp Gly Lys  
 195 200 205  
 His Gly Val Leu Thr Trp Leu Arg Glu Asn Pro Gly Gly Ser Glu Glu  
 210 215 220  
 Ser Leu Arg Lys Leu Pro Gly Pro Leu Pro Pro Ala Gly Ser Leu Gln  
 225 230 235 240  
 Thr Ser Val Thr Pro Arg Pro Ser Trp Ala Glu Ala Pro Trp Leu Val  
 245 250 255  
 Gly Gly Gln Pro Ala Leu Trp Ser Ile Leu Leu Met Pro Pro Arg Tyr  
 260 265 270  
 Gly Ile Pro Phe Tyr His Ser Thr Pro Thr Thr Gly Ala Trp Gln Glu  
 275 280 285  
 Val Trp Arg Glu Gln Arg Ile Pro Leu Ser Leu Asn Ala Pro Lys Gly  
 290 295 300  
 Leu Trp Ser Gln Asn Gln Leu Ala Ser Ser Ser Pro Thr Pro Gly Ser  
 305 310 315 320  
 Leu Pro Gln Gly Pro Ala Gln Leu Ser Pro Gly Glu Met Glu Glu Ser  
 325 330 335  
 Asp Gln Gly His Thr Gly Ala Leu Ala Thr Cys Ala Gly His Glu Asp  
 340 345 350  
 Lys Ala Gly Cys Pro Pro Arg Pro His Pro Pro Pro Ala Pro Pro Ala  
 355 360 365  
 Arg Ser Arg Pro Tyr Ala Cys Ser Val Cys Gly Lys Arg Phe Ser Leu  
 370 375 380  
 Lys His Gln Met Glu Thr His Tyr Arg Val His Thr Gly Glu Lys Pro  
 385 390 395 400  
 Phe Ser Cys Ser Leu Cys Pro Gln Arg Ser Arg Asp Phe Ser Ala Met  
 405 410 415  
 Thr Lys His Leu Arg Thr His Gly Ala Ala Pro Tyr Arg Cys Ser Leu  
 420 425 430  
 Cys Gly Ala Gly Cys Pro Ser Leu Ala Ser Met Gln Ala His Met Arg  
 435 440 445  
 Gly His Ser Pro Ser Gln Leu Pro Pro Gly Trp Thr Ile Arg Ser Thr  
 450 455 460

Phe Leu Tyr Ser Ser Ser Arg Pro Ser Arg Pro Ser Thr Ser Pro Cys  
 465 470 475 480

Cys Pro Ser Ser Ser Thr Thr  
 485

<210> 12  
 <211> 2436  
 <212> DNA  
 <213> Homo sapiens

<400> 12  
 caacaacccat ctacagctgt attcttctgtc ccttgatggc acaattaaac tgtgggacta 60  
 tatagatggc atcttaataa agactttcat agttggatgc aaacttcatg cctcttttac 120  
 tcttgcccaa gctgaggatt ctgtctttgt tatagtgaat aaagaaaaac cagatatatt 180  
 tcagctgggt tcagtgaaac tgccaaaac ctcaagccag gaagtagaag ccaaggagct 240  
 gtcccttgggt ttggattaca taaaccagtc acccaagtgc attgcctttg gaaacgaggg 300  
 agtatatggt gctgcagtac gggaatttta cttgtctgtt tattttttca aaaagaaaac 360  
 aacatcaagg ttactttat catcatcaag aaataagaag catgctaaaa acaattttac 420  
 gtgtgtagca tgtcacccaa cggaagactg catcgcatct ggtcacatgg atggcaaaat 480  
 tcgtctttgg aggaattttt atgatgataa gaaatatacg tacacatgtt tacattggca 540  
 ccatgatatg gttatggatt tggctttttc agtgacaggc accagtctgc tgagtggcgg 600  
 tcgtgaatct gtactttag agtggcgaga tgcaacagag aagaataagg agtttctccc 660  
 gcgttttaga gctactattg aacatatctc agtctcgcc gcaggagatt tattctgcac 720  
 ttctcactct gataataaga taataattat tcaccgaaac ctgaagcat ccgcagtaat 780  
 tcaaggccca gtgaaagata ggagtatctt cactggtttg atgattgac caagaactaa 840  
 agctttgggt ttgaatggaa aacctggcca cctgcagtct tattctctcc agagtataa 900  
 acagttatcc aatttagata ttatacagca agaataatatt aatgattatg gtctgatcca 960  
 aattgaacta acaaaggctg catttggctg ctttggtaac tggcttgcaa cagtggaaac 1020  
 ggggcaagaa aaggaaactg agcttgaatt gcaaatgaaa ctgtggatgt ataataagaa 1080  
 aacacaaggg ttatttctta acactaaaat taacatgcca cacgaagact gcattacagc 1140  
 tctctgtttc tgtaatgcag aaaaacttga acagccacc ttggttacag ctagcaaaaga 1200  
 tggttacttc aaagtatgga tattaacaga tgactctgac atatacaaaa aagctgttgg 1260  
 ctggacctgt gactttgttg gtagttatca caagtatcaa gcaactaact gttgtttctc 1320  
 cgaagatggt tctttactag cagttagttt tgaggaaata gtcacaatat gggattctgt 1380  
 aacatgggaa cttaaatgta cattttgcc aagagctggg aaaataaggc acctttgctt 1440  
 tgggagattg acgtgttcaa agtatctact tgggtgctact gaaaatggca ttctttgctg 1500  
 ttggaatctg ctgagctgtg cattggagtg gaatgcaaaa ttaaatgtta gaggatgga 1560  
 acccgatcct aattcagaga atattgctgc aatctctcag tcttcagtgg gttcagactt 1620  
 gtttgtatct aaacctagt agccaaggcc attgtatat caaaagggtta tctccagaga 1680  
 gaaagtccag tggggagtggt ttgttccacg agatgtccct gaatccttca cctcagaagc 1740  
 ttaccagtgg ctaaatagat ccagttttta cttcctaaca aaatcacaga gtttattgac 1800  
 attcagtaca agtctccag aagaaaaact cacaccaaca agcaaacagc tgctagcaga 1860  
 agaaagtctt ccacaaccc cattttattt catattggga aaacacaggg aacagcagga 1920  
 tgaaaaacta aacgaaactt tagagaatga gctggtacaa ctacccttaa cagaaaacat 1980  
 acccgcaatt agtgagcttc ttcacactcc agcccatgtc ctgccatctg ctgctttctt 2040  
 gtgctccatg ttgttaaatt cattgctgct gtctaaagag actaagagtg ctaaggaaat 2100  
 tcctgaagat gtagatatgg aagaagaaaa agaaagtga gattcagatg aagaaaatga 2160  
 ttttaccgaa aaagtccagg atacaagtaa cacaggttta ggagaagaca ttatacatca 2220  
 gttgtcaaaa ttgaagaaa aagaactgag aaaatttagg aaaatagact acagctggat 2280  
 agctgccctt taagccttgg agatggggag gatccttggg ctttctgttt ttgattgtat 2340  
 gttgatattc taaaaacatc tattttaatg ttatttctgt tctaaaaata agataataaa 2400  
 tattaacaaa ctttaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 13  
 <211> 763  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 13

Asn Asn His Leu Gln Leu Tyr Ser Cys Ser Leu Asp Gly Thr Ile Lys  
 1 5 10 15  
 Leu Trp Asp Tyr Ile Asp Gly Ile Leu Ile Lys Thr Phe Ile Val Gly  
 20 25 30  
 Cys Lys Leu His Ala Leu Phe Thr Leu Ala Gln Ala Glu Asp Ser Val  
 35 40 45  
 Phe Val Ile Val Asn Lys Glu Lys Pro Asp Ile Phe Gln Leu Val Ser  
 50 55 60  
 Val Lys Leu Pro Lys Ser Ser Ser Gln Glu Val Glu Ala Lys Glu Leu  
 65 70 75 80  
 Ser Phe Val Leu Asp Tyr Ile Asn Gln Ser Pro Lys Cys Ile Ala Phe  
 85 90 95  
 Gly Asn Glu Gly Val Tyr Val Ala Ala Val Arg Glu Phe Tyr Leu Ser  
 100 105 110  
 Val Tyr Phe Phe Lys Lys Lys Thr Thr Ser Arg Phe Thr Leu Ser Ser  
 115 120 125  
 Ser Arg Asn Lys Lys His Ala Lys Asn Asn Phe Thr Cys Val Ala Cys  
 130 135 140  
 His Pro Thr Glu Asp Cys Ile Ala Ser Gly His Met Asp Gly Lys Ile  
 145 150 155 160  
 Arg Leu Trp Arg Asn Phe Tyr Asp Asp Lys Lys Tyr Thr Tyr Thr Cys  
 165 170 175  
 Leu His Trp His His Asp Met Val Met Asp Leu Ala Phe Ser Val Thr  
 180 185 190  
 Gly Thr Ser Leu Leu Ser Gly Gly Arg Glu Ser Val Leu Val Glu Trp  
 195 200 205  
 Arg Asp Ala Thr Glu Lys Asn Lys Glu Phe Leu Pro Arg Leu Gly Ala  
 210 215 220  
 Thr Ile Glu His Ile Ser Val Ser Pro Ala Gly Asp Leu Phe Cys Thr  
 225 230 235 240  
 Ser His Ser Asp Asn Lys Ile Ile Ile Ile His Arg Asn Leu Glu Ala  
 245 250 255  
 Ser Ala Val Ile Gln Gly Leu Val Lys Asp Arg Ser Ile Phe Thr Gly  
 260 265 270  
 Leu Met Ile Asp Pro Arg Thr Lys Ala Leu Val Leu Asn Gly Lys Pro  
 275 280 285  
 Gly His Leu Gln Phe Tyr Ser Leu Gln Ser Asp Lys Gln Leu Tyr Asn  
 290 295 300  
 Leu Asp Ile Ile Gln Gln Glu Tyr Ile Asn Asp Tyr Gly Leu Ile Gln  
 305 310 315 320

Ile Glu Leu Thr Lys Ala Ala Phe Gly Cys Phe Gly Asn Trp Leu Ala  
 325 330 335  
 Thr Val Glu Gln Arg Gln Glu Lys Glu Thr Glu Leu Glu Leu Gln Met  
 340 345 350  
 Lys Leu Trp Met Tyr Asn Lys Lys Thr Gln Gly Phe Ile Leu Asn Thr  
 355 360 365  
 Lys Ile Asn Met Pro His Glu Asp Cys Ile Thr Ala Leu Cys Phe Cys  
 370 375 380  
 Asn Ala Glu Lys Ser Glu Gln Pro Thr Leu Val Thr Ala Ser Lys Asp  
 385 390 395 400  
 Gly Tyr Phe Lys Val Trp Ile Leu Thr Asp Asp Ser Asp Ile Tyr Lys  
 405 410 415  
 Lys Ala Val Gly Trp Thr Cys Asp Phe Val Gly Ser Tyr His Lys Tyr  
 420 425 430  
 Gln Ala Thr Asn Cys Cys Phe Ser Glu Asp Gly Ser Leu Leu Ala Val  
 435 440 445  
 Ser Phe Glu Glu Ile Val Thr Ile Trp Asp Ser Val Thr Trp Glu Leu  
 450 455 460  
 Lys Cys Thr Phe Cys Gln Arg Ala Gly Lys Ile Arg His Leu Cys Phe  
 465 470 475 480  
 Gly Arg Leu Thr Cys Ser Lys Tyr Leu Leu Gly Ala Thr Glu Asn Gly  
 485 490 495  
 Ile Leu Cys Cys Trp Asn Leu Leu Ser Cys Ala Leu Glu Trp Asn Ala  
 500 505 510  
 Lys Leu Asn Val Arg Val Met Glu Pro Asp Pro Asn Ser Glu Asn Ile  
 515 520 525  
 Ala Ala Ile Ser Gln Ser Ser Val Gly Ser Asp Leu Phe Val Phe Lys  
 530 535 540  
 Pro Ser Glu Pro Arg Pro Leu Tyr Ile Gln Lys Gly Ile Ser Arg Glu  
 545 550 555 560  
 Lys Val Gln Trp Gly Val Phe Val Pro Arg Asp Val Pro Glu Ser Phe  
 565 570 575  
 Thr Ser Glu Ala Tyr Gln Trp Leu Asn Arg Ser Gln Phe Tyr Phe Leu  
 580 585 590  
 Thr Lys Ser Gln Ser Leu Leu Thr Phe Ser Thr Lys Ser Pro Glu Glu  
 595 600 605  
 Lys Leu Thr Pro Thr Ser Lys Gln Leu Leu Ala Glu Glu Ser Leu Pro  
 610 615 620  
 Thr Thr Pro Phe Tyr Phe Ile Leu Gly Lys His Arg Gln Gln Gln Asp  
 625 630 635 640

Glu Lys Leu Asn Glu Thr Leu Glu Asn Glu Leu Val Gln Leu Pro Leu  
                   645                                  650                                  655  
 Thr Glu Asn Ile Pro Ala Ile Ser Glu Leu Leu His Thr Pro Ala His  
                   660                                  665                                  670  
 Val Leu Pro Ser Ala Ala Phe Leu Cys Ser Met Phe Val Asn Ser Leu  
                   675                                  680                                  685  
 Leu Leu Ser Lys Glu Thr Lys Ser Ala Lys Glu Ile Pro Glu Asp Val  
                   690                                  695                                  700  
 Asp Met Glu Glu Glu Lys Glu Ser Glu Asp Ser Asp Glu Glu Asn Asp  
                   705                                  710                                  715                                  720  
 Phe Thr Glu Lys Val Gln Asp Thr Ser Asn Thr Gly Leu Gly Glu Asp  
                   725                                  730                                  735  
 Ile Ile His Gln Leu Ser Lys Ser Glu Glu Lys Glu Leu Arg Lys Phe  
                   740                                  745                                  750  
 Arg Lys Ile Asp Tyr Ser Trp Ile Ala Ala Leu  
                   755                                  760

<210> 14  
 <211> 137  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (2)

<220>  
 <221> unsure  
 <222> (18)  
 <220>  
 <221> unsure  
 <222> (29)..(30)

<220>  
 <221> unsure  
 <222> (36)

<220>  
 <221> unsure  
 <222> (44)

<220>  
 <221> unsure  
 <222> (49)

<220>  
 <221> unsure  
 <222> (62)

<220>

<221> unsure  
<222> (67)

<220>  
<221> unsure  
<222> (80)

<220>  
<221> unsure  
<222> (93)

<220>  
<221> unsure  
<222> (99)

<220>  
<221> unsure  
<222> (108)

<220>  
<221> unsure  
<222> (112)

<220>  
<221> unsure  
<222> (121)

<400> 14  
gngggggagg atgaatantc ggaagctggn gggcngcggy gganccaang aagagggtcc 60  
gnaccngct tacgaaccgn ggactcttga ctncaccacnc cctgaacnct cncctccaaa 120  
ngcgtcatgg atggaat 137

<210> 15  
<211> 539  
<212> DNA  
<213> Homo sapiens

<400> 15  
gtggaggagg agtgaattct gggaatctct cagcagcttt ttgccaaaca gatggggccag 60  
gagccgcgga accaggctga ggaatgttgc ctcacgatct ctcatatcca ttcctggcac 120  
ccaccagccc agggaatgcc tctaccagtt gtcagcgaga ggcttacaca gcatcttaaa 180  
taaaagggat tattgaacca agaggccagg gactgatgga aatgcccacc ttgctggctc 240  
attgaaaaag tttggcaagg ttgtcaggag acatgaatta gatgggcttg ggtcttgtgc 300  
cctttgctaa accaagtgtc gtattgggaa agagacgggg agagaagtgt tggagatgct 360  
ctttagtcag gcctgagtca cttgcccac cctggagttg gaggttggga tggagccagg 420  
atctccaaac cacatgcccc tagagtttca gggaaaatat ggattgtgaa ttgaagatgg 480  
ggggtgatgt aaggcagaca aggacagaaa atccctcttc cagctgtgat ttggctgtg 539

<210> 16  
<211> 27  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Asp Cys Glu Leu Lys Met Gly Gly Asp Val Arg Gln Thr Arg Thr  
1 5 10 15  
Glu Asn Pro Ser Ser Ser Cys Asp Leu Ala Val  
20 25



<210> 17  
 <211> 99  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (50)

<220>  
 <221> unsure  
 <222> (55)..(56)

<220>  
 <221> unsure  
 <222> (62)

<220>  
 <221> unsure  
 <222> (64)

<220>  
 <221> unsure  
 <222> (84)

<400> 17  
 agagaggcag atccccaatg aggggtcagg acgggtcttg gctgcacatn ctggnnntcat 60  
 antnatccca tggggagcag cacnttatga aaaaaaaaaa 99

<210> 18  
 <211> 2608  
 <212> DNA  
 <213> Homo sapiens

<400> 18  
 attagccact gcacctggct ggtgtctcca ttttacagat gaggtgtgca cccccaata 60  
 tcacacagcc aagtggcaga gttgtgttca aatgctggca gtcaggccat gctctgtctg 120  
 artccaract ctgccacttt ctarctgtgt gttctcgggc aggttatatta ccaactttga 180  
 agtccatttt cttatcccta aaagagggct gagaagctca cccctacctt tgaaggttgt 240  
 ttgaggatta agcaagacca gcatctgaag ggcctgaagc atctagggca tcatcagtgc 300  
 actttatctc tggcctctaa gaagtgcac tagaaggagc ccactgtcac agcttccctg 360  
 tacccttgcc ttgacctgac aggtagcact tcgggtttgga cctcactttt tcaggatttg 420  
 ttggaaacaa gatcccttat cttctctagg tcagatttgg ggtgaacttg gctgacagta 480  
 ttccagggca ggcagaggtc aggtctggctg gtgacctgct gcctccttcc catcggcagc 540  
 tagttctagg gccatccaca gggatcccca gccctccata gtaccagtga gcctcactgg 600  
 catgtgccag ggccaagagg gccttcagcg tcgctccag tccagccctg tctcgtatt 660  
 cttggggaca ctgtggtca gccagcacag tgcctagccc acagtcaccc agcaggcgtc 720  
 cctcgagtgg gccagtggca ggcacagagc tgcctcctcc ttgctggat gcgtgaggaa 780  
 aggaactctt ctccctgcag cccagccctg caggctctct gctgccagat gacgagtga 840  
 gatgaaagtc ctgatgtcta ttgtctgtgt gcacagagct ttggagtggc ctggccagga 900  
 agagggggaag cgtgtgtggg gtcagcaca ggggttgccg ggtctcttgg tactggttct 960  
 gctctgtctg tggttccctc tgaaaatgtg ggtttctccc ctccgtgctg agcctcagaa 1020  
 agggggcagg agccccatgc cagcacacat ggccccctcg ctctctggcc tctgcagggt 1080  
 cagcccagct ccttcacctc tctcctgctt tccccctcagg cctcagtgc cccacacccc 1140  
 cttcaggccc aagcctggat ggtaccggat ggaacagctt ccagtctgct gatgccactg 1200  
 agccccccag cccctgctct ggcccaggcc cccagtatgg aaagccgacc cccagcgag 1260  
 acatccctgc cagcaagcag cggctctggac gacctagacc tcttggggaa gacctcctg 1320  
 cagcagctgc tgcccccgga atcccagcaa gtgctgtggg agaagcagca gccaaccccc 1380  
 cggctcacac tccgggacct gcagaataag agcagcagct gcagctcccc cagctccagc 1440

```

gccaccagcc ttctccacac cgtgtcccca gagcccccca ggctccgca gcagcccgta 1500
ccaaccgagc tctcactggc cagcatcact gtgcccctgg agtccatcaa acccagcaac 1560
atcctgcccg tgactgtgta tgaccagcac ggcttccgca tctctttcca ttttgcccgg 1620
gacccactgc cagggcgctc cgacgtgctg gtggtggtgg tttccatgct gagcaccgcc 1680
ccccagccca tccgcaacat cgtgttccag tcagctgtcc ccaaggttat gaagggtgaag 1740
ctgcagccac cctcgggcac ggagctgcca gcttttaacc ccatcgctca ccctcagca 1800
atcaccagcgc tctgtctgct tgccaacccc cagaaggaga aggttcgcct ccgctacaag 1860
ctcaccttca ccatgggtga ccagacctac aacgagatgg gggatgtgga ccagttcccc 1920
ccacctgaaa cctggggtag cctctagaac agaggggctg gggagaggaa ggggcagagg 1980
gaccgggtcac tgtccagcct ggaggggaggc attggtggcc aaggacaccc tttgttgccc 2040
atggccattc acccccaggc ctggtgcttc tccccacacc cctgtaggcc tcaagtgact 2100
cttccccctc ctgctccggc cccgcccctg ctgagccaaa cccagtagga ggctgggctt 2160
gggtttgtgc cgtcggggtc tccatcaccc ggacctggag agggaggggc tgtgtagcct 2220
tggaagaact tgggtcatgg ggaggaagca cagctgttgg ggaagggccca ggacctcagg 2280
cccagcccca accccagctg ggggtgggtc tccccacct gtctcttatg ctttatggga 2340
aggcccagcc ataactcggg ggccatgctc gagctgggga ccagcttagg cctcctatgg 2400
gtgtcttacg tctgtccatc catctgtccg tggtcagaag tggggtcagt gtgtgagtga 2460
gagcaggagt atttatgaaa ataaaacgtc gtttttcctg gaaaaaaaaa aaaaaaaaaa 2520
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2580
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

```

<210> 19  
 <211> 236  
 <212> PRT  
 <213> Homo sapiens

```

<400> 19
Met Glu Ser Arg Pro Pro Ala Gln Thr Ser Leu Pro Ala Ser Ser Gly
  1             5             10             15

Leu Asp Asp Leu Asp Leu Leu Gly Lys Thr Leu Leu Gln Gln Ser Leu
  20             25             30

Pro Pro Glu Ser Gln Gln Val Arg Trp Glu Lys Gln Gln Pro Thr Pro
  35             40             45

Arg Leu Thr Leu Arg Asp Leu Gln Asn Lys Ser Ser Ser Cys Ser Ser
  50             55             60

Pro Ser Ser Ser Ala Thr Ser Leu Leu His Thr Val Ser Pro Glu Pro
  65             70             75             80

Pro Arg Pro Pro Gln Gln Pro Val Pro Thr Glu Leu Ser Leu Ala Ser
  85             90             95

Ile Thr Val Pro Leu Glu Ser Ile Lys Pro Ser Asn Ile Leu Pro Val
 100             105             110

Thr Val Tyr Asp Gln His Gly Phe Arg Ile Leu Phe His Phe Ala Arg
 115             120             125

Asp Pro Leu Pro Gly Arg Ser Asp Val Leu Val Val Val Val Ser Met
 130             135             140

Leu Ser Thr Ala Pro Gln Pro Ile Arg Asn Ile Val Phe Gln Ser Ala
 145             150             155             160

Val Pro Lys Val Met Lys Val Lys Leu Gln Pro Pro Ser Gly Thr Glu
 165             170             175

```

Leu Pro Ala Phe Asn Pro Ile Val His Pro Ser Ala Ile Thr Gln Val  
180 185 190

Leu Leu Leu Ala Asn Pro Gln Lys Glu Lys Val Arg Leu Arg Tyr Lys  
195 200 205

Leu Thr Phe Thr Met Gly Asp Gln Thr Tyr Asn Glu Met Gly Asp Val  
210 215 220

Asp Gln Phe Pro Pro Pro Glu Thr Trp Gly Ser Leu  
225 230 235

<210> 20

<211> 328

<212> DNA

<213> Homo sapiens

<400> 20

agacttcgaa ttcggccttc atggcctara aaaactgatt cacctggcag agacctaccc 60  
catccacatg cacagccagc tggaccacct tagcctctat tactgcaggt gtactctgcc 120  
agagaatcca aacaatcaca cctccagta ctggaaggac cacaacatcg tgacagcaga 180  
agtccactgg gctaacctga ctgtcagtga atgccaggag atgcatggag agttcatggg 240  
atctgcgtgc ggccatcatg gaccctacac tctgatgtc ctcttttggg cctgtattct 300  
ctttttcacc accttcaccc tctcaagc 328

<210> 21

<211> 87

<212> PRT

<213> Homo sapiens

<400> 21

Met His Ser Gln Leu Asp His Leu Ser Leu Tyr Tyr Cys Arg Cys Thr  
1 5 10 15

Leu Pro Glu Asn Pro Asn Asn His Thr Leu Gln Tyr Trp Lys Asp His  
20 25 30

Asn Ile Val Thr Ala Glu Val His Trp Ala Asn Leu Thr Val Ser Glu  
35 40 45

Cys Gln Glu Met His Gly Glu Phe Met Gly Ser Ala Cys Gly His His  
50 55 60

Gly Pro Tyr Thr Pro Asp Val Leu Phe Trp Ser Cys Ile Leu Phe Phe  
65 70 75 80

Thr Thr Phe Ile Leu Ser Ser  
85

<210> 22

<211> 326

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1)

<220>  
 <221> unsure  
 <222> (31)

<220>  
 <221> unsure  
 <222> (82)

<220>  
 <221> unsure  
 <222> (84)

<220>  
 <221> unsure  
 <222> (129)

<400> 22  
 naaatgtatt tatatgtatg tcttattata nacaaggcag atttccctg gaataaaagt 60  
 ctagaatgta ctgcttaatt tnanacatgt gtgcaggcaa tattatctgt gagtgaaaag 120  
 tggaaataana cgtggattgg gtcaactgat tatcagcttg ttaggagtc tctgtgtgag 180  
 acatgggtggt ataattgtga agttctcact gtatgtggat gttcatgtga aagatagtag 240  
 tttcttcccg taaatatctt ttgatttcca tttgtatgga atcccaatga atgtatcttt 300  
 ggaaaacaaa aaaaaaaaaa aaaaaa 326

<210> 23  
 <211> 194  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (55)

<220>  
 <221> unsure  
 <222> (73)

<220>  
 <221> unsure  
 <222> (119)

<220>  
 <221> unsure  
 <222> (126)

<220>  
 <221> unsure  
 <222> (137)

<220>  
 <221> unsure  
 <222> (174)

<400> 23  
 aagtctcatt ctcaagagtg atgctgcaaa accccttttg ggccatgatg ctgtnatcca 60  
 ggcttttagca canaaaggtc tttatgtcac tgaccaggaa aaattggtaa ctgaacgana 120  
 tctccncaag aaacccttac agatgagtgc acatttgggc catgatcgat accncatgat 180  
 ggcttatact gtat 194

<210> 24

<211> 396  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (139)

<400> 24  
 ttcattttta ctgtcctgat gttgtcagat tagaggatat ttgtttgaaa gaaactatgt 60  
 ctttggttga tagcctgtat aatctgcagc tgattcaaga attttgcaa gaatacttga 120  
 accagtgttg ccatttcant ctggaagata tgctctatgc tgcttcatcc ataaagagta 180  
 attatttggt gttcatggcg gaactgttct ggtgggttga agtgggtgaag ccgtcttttg 240  
 tacagcctcg tgttgttcgt ccacaaggag ctgaacctgt aaaagatatg ccttcaattc 300  
 ctgtcttgaa tgctgcaaaa agaaatgtct tagatagtag ttctgacttc ccttcaagtg 360  
 ggggaaggagc tacatttaca cagtccatc tcgagg 396

<210> 25  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (28)

<400> 25  
 Met Ser Leu Ala Asp Ser Leu Tyr Asn Leu Gln Leu Ile Gln Glu Phe  
 1 5 10 15  
 Cys Gln Glu Tyr Leu Asn Gln Cys Cys His Phe Xaa Leu Glu Asp Met  
 20 25 30  
 Leu Tyr Ala Ala Ser Ser Ile Lys Ser Asn Tyr Leu Val Phe Met Ala  
 35 40 45  
 Glu Leu Phe Trp Trp Phe Glu Val Val Lys Pro Ser Phe Val Gln Pro  
 50 55 60  
 Arg Val Val Arg Pro Gln Gly Ala Glu Pro Val Lys Asp Met Pro Ser  
 65 70 75 80  
 Ile Pro Val Leu Asn Ala Ala Lys Arg Asn Val Leu Asp Ser Ser Ser  
 85 90 95  
 Asp Phe Pro Ser Ser Gly Glu Gly Ala Thr Phe Thr Gln Ser His Leu  
 100 105 110

Glu

<210> 26  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (87)

<220>  
 <221> unsure  
 <222> (123)

<400> 26  
 aatttgatga tgaccagaaa gtatgctgtg gttctttttt aaggatgac aaaaagcaga 60  
 aaatgatatg gcaatgaaac gggcagnttt gttggagaaa agattaagaa gggaaaagga 120  
 aantcagctc cggaacaac agttggaagc agaaatggag cataagaagg aggaaacaag 180  
 gcgtaaaact gaggaagaac gtcagaagaa agaagatgag agagcacgca gagaatttat 240  
 taggcaagaa tataatgaggc ggaaacaact gaaactaatg gaagatatgg atacagtaat 300  
 taaaccccggt cctcaagtag taaaaaaaaa aaaaaa 336

<210> 27  
 <211> 917  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 cacctggatt atctcagtag tttcccaact ggtttccttg tttccattct tgcctccttc 60  
 tgtctactct caatataaca gctagaacaa tccttttaca atggaattca gatcatgttt 120  
 acccctctgt tcaaattctc cagtgaacttt ccagttttta catgatctgg ctctactac 180  
 ctgtctcact gtgtttccta ctactctcct gccctttctc ctcttaataa acactgggct 240  
 catggtgttt cctttaacat gccaggcatg cttgacctg tcctgtctca gggccctgct 300  
 gttccctctg cctggaacat tcttcccata gtgtctgcat ggctcgtctt ctcactgctt 360  
 tggattgctg ctcaaaagtc accttatcaa aggccttttc caaagggtta aaaatcattc 420  
 tactataaag acacatgcat acatatgttt attgcagcac tattcacaat aacaaagact 480  
 tggaaaccaac ccaaagccc atcaatgata gactggataa agaaaatatg gcacgtaagc 540  
 accatggaat actatgcagc cataaaaaag aatgagttca tgtcctttgc agggacatgg 600  
 atgaagctgg aaaccattat tctcagcaaa ctaacacagg aacagaaaac caaacaccgc 660  
 atgttctcac tcataagtgg gagttgaaca atgagaacat acgggcacag tggggggaac 720  
 atcacacacc agggcctgtc ggggggtgag aggcaaggga agtgatagca ttaagagaaa 780  
 tacctaagt agattatggg ttgatggggg cagcaaacca ccatggcaca tgtgtacctt 840  
 tgtaacaaac ctgcacattc tgcacatata tcccagaact taaagtataa ttaaagaaaa 900  
 agaaaaaaaa aaaaaa 917

<210> 28  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Met Glu Phe Arg Ser Cys Leu Pro Leu Cys Ser Asn Ser Pro Val Thr  
 1 5 10 15  
 Phe Gln Phe Leu His Asp Leu Ala Pro Thr Thr Cys Leu Thr Val Phe  
 20 25 30  
 Pro Thr Thr Leu Leu Pro Phe Leu Leu Leu Ile Asn Thr Gly Leu Met  
 35 40 45  
 Val Phe Pro Leu Thr Cys Gln Ala Cys Leu Thr Leu Ser Cys Leu Arg  
 50 55 60  
 Ala Leu Leu Phe Pro Leu Pro Gly Thr Phe Phe Pro  
 65 70 75

<210> 29  
 <211> 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

```

ggctttgacc gctatcgcca ggagtggatg gactatggct gtgcacagga ggcagagggc 60
aggatgtgcg aggacttcca ggatgaggac cacgactcag cctccccctga cacttccttc 120
agccccctatg atggagacct caccamtacc tcctcctccc tcttcacga cagcctcacc 180
acagaagatg acaccaagtt gaatccctat gcaggaggag acggccttca gaacaacctg 240
tcccccaaga caaagggcac tcctgtgcac ctgggcacca tcgtgggcat cgtgctggca 300
gtcctcctcg tggcgggccat catcctggct ggaatttaca tcaatggcca c 351

```

&lt;210&gt; 30

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (40)

&lt;400&gt; 30

```

Met Asp Tyr Gly Cys Ala Gln Glu Ala Glu Gly Arg Met Cys Glu Asp
 1             5             10             15
Phe Gln Asp Glu Asp His Asp Ser Ala Ser Pro Asp Thr Ser Phe Ser
          20             25             30
Pro Tyr Asp Gly Asp Leu Thr Xaa Thr Ser Ser Ser Leu Phe Ile Asp
          35             40             45
Ser Leu Thr Thr Glu Asp Asp Thr Lys Leu Asn Pro Tyr Ala Gly Gly
          50             55             60
Asp Gly Leu Gln Asn Asn Leu Ser Pro Lys Thr Lys Gly Thr Pro Val
          65             70             75             80
His Leu Gly Thr Ile Val Gly Ile Val Leu Ala Val Leu Leu Val Ala
          85             90             95
Ala Ile Ile Leu Ala Gly Ile Tyr Ile Asn Gly His
          100             105

```

&lt;210&gt; 31

&lt;211&gt; 179

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (24)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (33)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (56)

<220>  
<221> unsure  
<222> (82)

<220>  
<221> unsure  
<222> (93)

<220>  
<221> unsure  
<222> (99)

<220>  
<221> unsure  
<222> (117)

<220>  
<221> unsure  
<222> (137)

<400> 31  
gttggtcagcc ccttcctttc ccngaccta aanataaaa acaaggcaaa gcccgnataa 60  
ttttaagacg gttttttagg anattagtc acnattttnt tggtttgatg gttttcngaa 120  
ataaagtccc tttcctngct ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 179

<210> 32  
<211> 3906  
<212> DNA  
<213> Homo sapiens

<400> 32  
ggaaactcag ccacctgtga caaatttgag tgtctctggt gaaaacctct gcacagtaat 60  
atggacatgg aatccacccg agggagccag ctcaaattgt agtctatggt attttagtca 120  
ttttggcgac aaacaagata agaaaatagc tccggaaact cgtcgttcaa tagaagtacc 180  
cctgaatgag aggatttgte tgcaagtggg gtccagtggt agcaccaatg agagtggaga 240  
gcctagcatt ttggttgaaa aatgcattct acccccagaa ggtgatcctg agtctgctgt 300  
gactgagctt caatgcattt ggcacaacct gagctacatg aagtgttctt ggctccctgg 360  
aaggaatacc agtcccagca ctaactatac tctctactat tggcacagaa gcctggaaaa 420  
aattcatcaa tgtgaaaaca tcttttagaga aggccaatat ttgggttggt cctttgatct 480  
gaccaaagtg aaggattcca gttttgaaca acacagtggt caaataatgg tcaaggataa 540  
tgagggaaaa attaaacat ccttcaatat agtgccttta acttcccgtg tgaacctga 600  
tctccacat attaaaaacc tctccttcca caatgatgac ctatatgtgc aatgggagaa 660  
tccacagaat tttattagca gatgcctatt ttatgaagta gaagtcaata acagccaaac 720  
tgagacacat aatgttttct acgtccaaga ggctaaatgt gagaatccag aatttgagag 780  
aatgtggag aatacatctt gtttcatggt ccctgggtgt cttcctgata ctttgaacac 840  
agtcagaata agagtcaaaa caaataagtt atgctatgag gatgacaaac tctggagtaa 900  
ttggagccaa gaaatgagta taggtaagaa gcgcaattcc acactctaca taacctgtt 960  
actcattgtt ccagtcacgt tgcaggtgc aatcatagta ctctctgtt accataaaaag 1020  
gctcaagatt attatattcc ctccaattcc tgatcctggc aagattttta aagaaatgtt 1080  
tggagaccag aatgatgata ctctgcactg gaagaagtac gacatctatg agaagcaaac 1140  
caaggaggaa accgactctg tagtgctgat agaaaacctg aagaaagcct ctcaagtgat 1200  
gagataatct atttttacct tcaactgtgac cttgagaaga ttcttcccat tctccatttg 1260  
ttatctggga acttattaaa tggaaactga aactactgca ccatttaaaa acaggcagct 1320  
cataagagcc acaggtcttt atgttgagtc gcgcaccgaa aaactaaaaa taatggggcg 1380  
tttgaggaga agtgtggagt cattctcatt gaattataaa agccagcagg cttcaaaacta 1440  
ggggacaaa gcaaaaagtga tgataatggt ggagttaate ttatcaagag ttgtgacaac 1500  
ttcctgaggg atctatactt gctttgtgtt ctttgtgtca acatgacaa attttatttg 1560  
taggggaact catttggggt gcaaatgcta atgtcaaaact tgagtcaaa agaacatgta 1620  
gaaaacaaaa tggataaaat ctgatatgta ttgtttggga tcctattgaa ccattgtttg 1680  
ggctattaaa actcttttaa cagctcgggc tgggtccggg ggctcacgc tgtaatccca 1740



gcaatttggg agtccgaggc gggcggatca ctcgaggtca ggagttccag accagcctga 1800  
 ccaaaatggt gaaacctcct ctctactaaa actacaaaaa ttaactgggt gtggtggcgc 1860  
 gtgcctgtaa tcccagctac tcgggaagct gaggcaggtg aattgtttga acctgggagg 1920  
 tggaggttgc agtgagcaga gatcacacca ctgcactcta gcctgggtga cagagcaaga 1980  
 ctctgtctaa aaaacaaaac aaaacaaaac aaaacaaaaa aacctcttaa tattctggag 2040  
 tcatcattcc ctctgacagc attttctctt gctttgaaag cccagaaaat cagtgttggc 2100  
 catgatgaca actacagaaa aaccagaggc agcttctttg ccaagacctt tcaaagccat 2160  
 tttaggctgt taggggcagt ggaggtagaa tgactccttg ggtattagag tttaaccat 2220  
 gaagtctcta acaatgtatt ttcttcacct ctgctactca agtagcattt actgtgtctt 2280  
 tgggtttgtgc tagggccccc gggtgtgaagc acagaccctt tccaggggtt tacagtctat 2340  
 ttgagactcc tcagttcttg ccactttttt tttaactctc accagtcatt ttccagacct 2400  
 tttaactcct caattccaac actgatttcc ccttttgcct tctcctcctt tcccttcctt 2460  
 gtagcctttt gactttcatt ggaaattagg atgtaaatct gctcaggaga cctggaggag 2520  
 cagaggataa ttagcatctc aggttaagtg tgagtaatct gagaacaat gactaattct 2580  
 tgcataattt gtaacttcca tgtgaggggt ttccagcattg atatttgtgc attttctaaa 2640  
 cagagatgag gtggtatctt cacgtagaac attggtattc gcttgagaaa aaaagaatag 2700  
 ttgaacctat ttctctttct ttacaagatg gggtccaggat tctctcttct tctgccataa 2760  
 atgattaatt aatatgcttt tgtgtcttct attggtagcc agccagccaa ggctctgtt 2820  
 atgcttttgg ggggcatata ttgggttcca ttctcaccta tccacacaac atatccgtat 2880  
 atatccctct tactcttact tcccccaaat ttaaagaagt atgggaaatg agaggcattt 2940  
 cccccacccc atttctctcc tcacacacag actcatatta ctggtaggaa cttgagaact 3000  
 ttatttccaa gttgttcaaa catttaccaa tcatattaat acaatgatgc tatttgcaat 3060  
 tctgtctct aggggagggg agataagaaa cctcactct ctacagggtt ggttacaagt 3120  
 ggcaacctgc ttccatggcc gtgtagaagc atggtgacct ggcttctctg aggaagctgg 3180  
 ggttcacatg aatggcagat gtaaagtatt tcttgaagtc agattgaggc tgggagacag 3240  
 ccgtagtaga tgttctactt tgttctgtct ttctctagaa agaataattt gtttctctgt 3300  
 ataggaatga gattaattcc ttccaggtta tttataaatt ctgggaagca aaacctatgc 3360  
 ctccccctag ccatttttct tgttatctta tttagatggc catgaagagg atgctgtgaa 3420  
 attcccaaca aacattgatg ctgacagtca tgcagctctg gagtggggaa gtgatctttt 3480  
 gttcccatcc tcttctttta gcagtaaaat agctgagggg aaaggagggg aaaagggaagt 3540  
 tatgggaata cctgtgtgtg ttgtgatccc taggtcttgg gagctcttgg aggtgtctgt 3600  
 atcagtggtt tccccatccc ctgtgggaaa ttagtaggct catttactgt tttaggtcta 3660  
 gcttatgtgg attttttcct aacatacyta agcaaaccga gtgtcaggat ggtaattctt 3720  
 attcttctgt tcagtttaagt ttttcccttc atctgggcac tgaagggata tgtgaaacaa 3780  
 tgttaacatt tttggtagtc ttcaaccagg gattgtttct gtttaacttc ttataggaaa 3840  
 gcttgagtaa aataaatatt gtctttttgt atgtcaccca aaaaaaaaaa aaaaaaaaaa 3900  
 aaaaaa 3906

&lt;210&gt; 33

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn  
 1 5 10 15

Tyr Thr Leu Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys  
 20 25 30

Glu Asn Ile Phe Arg Glu Gly Gln Tyr Leu Gly Cys Ser Phe Asp Leu  
 35 40 45

Thr Lys Val Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met  
 50 55 60

Val Lys Asp Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro  
 65 70 75 80

Leu Thr Ser Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser

85 90 95

Phe His Asn Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe  
100 105 110

Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr  
115 120 125

Glu Thr His Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro  
130 135 140

Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly  
145 150 155 160

Val Leu Pro Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn  
165 170 175

Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu  
180 185 190

Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu  
195 200 205

Leu Ile Val Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu  
210 215 220

Tyr Leu Lys Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro  
225 230 235 240

Gly Lys Ile Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu  
245 250 255

His Trp Lys Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr  
260 265 270

Asp Ser Val Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln  
275 280 285

<210> 34  
<211> 1605  
<212> DNA  
<213> Homo sapiens

<400> 34

acgctgacca tcacaggcac acagaggcac atccacctca catccacctc atacttggtg 60  
actctcaggg ttcagtcctt catcctatcc ctctctgac tgtgcctccc aataccttcc 120  
aagatgttta cagagaccct tctccctgtg cagttaggag tgtaaggcaa gagagccct 180  
acttcaggg gcagatcaag agctgagacc aaagatggc tatgttgctg accttgctc 240  
gtcctcctgc tgtcttaaac tatgatccct gctgcggtca ctgaagcct tccctgtgag 300  
cagtgggtg tgagagccag gcgtccctct gctgcccac tcagtggcaa ccccgggag 360  
ctgttttgc ctttgtggag cctcagcagt tccctcttcc agaactcact gccaagagcc 420  
ctgaacagga gccaccatgc agtgcttcag ctccattaag accatgatga tccctctcaa 480  
tttgcctac tttctgtgtg gtgcagccct gttggcagtg ggcattctgg tgtcaatcga 540  
tggggcatcc tttctgaaga tcttcgggac actgtcgtcc agtgccatgc agtttgtcaa 600  
cgtgggctac ttcctcatcg cagccggcgt tgtggtctt gctcttggtt tcttgggctg 660  
ctatgggtg aagactgaga gcaagtgtgc cctcgtgacg ttcttcttca tctcctcct 720  
catcttcatt gctgaggttg cagctgctgt ggtcgcttg gtgtacacca caatggctga 780  
gcacttcctg acgttgctgg tagtgctgc catcaagaaa gattatggtt cccaggaaga 840  
cttcactcaa gtgtggaaca ccaccatgaa agggctcaag tgctgtggtc tcaccaacta 900

tacggatttt gaggactcac cctacttcaa agagaacagt gcctttcccc cattctgttg 960  
 caatgacaac gtcaccaaca cagccaatga aacctgcacc aagcaaaagg ctcacgacca 1020  
 aaaagtagag ggttgcttca atcagctttt gtatgacatc cgaactaatg cagtcaccgt 1080  
 ggggtggttg gcagctggaa ttgggggcct cgagctggct gccatgattg tgtccatgta 1140  
 tctgtactgc aatctacaat aagtccactt ctgcctctgc cactactgct gccacatggg 1200  
 aactgtgaag aggcaccctg gcaagcagca gtgattgggg gaggggacag gatctaaca 1260  
 tgtcacttgg gccagaatgg acctgccctt tctgctccag acttgggggt agataggac 1320  
 cactcctttt aggcgatgcc tgactttcct tccattgggt ggtggatggg tggggggcat 1380  
 tccagagcct ctaaggtagc cagtctctgt gccattccc ccagtctatt aaacccttga 1440  
 tatgccccct aggcctagtgt gtgatcccag tgctctactg ggggatgaga gaaaggcatt 1500  
 ttatagcctg ggcataagtgt aaatcagcag agcctctggg tggatgtgta gaaggcatt 1560  
 caaatgcat aaacctgtta caatgttgaa aaaaaaaaaa aaaaa 1605

<210> 35

<211> 241

<212> PRT

<213> Homo sapiens

<400> 35

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
 20 25 30  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
 35 40 45  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
 50 55 60  
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65 70 75 80  
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile  
 85 90 95  
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
 100 105 110  
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys  
 115 120 125  
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met  
 130 135 140  
 Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp  
 145 150 155 160  
 Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn  
 165 170 175  
 Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala  
 180 185 190  
 His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile  
 195 200 205  
 Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly  
 210 215 220

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
 225 230 235 240

Gln

<210> 36  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (346)

<400> 36  
 caacctcgtg gtcaccgcac cggggctgat caagggtgac gcctgcttca catctctaat 60  
 gaacaccctc atgacgtcgc taccagcact agtgcagcaa caggggaaggc tgcttctggc 120  
 tgctaattgtg gccaccctgg ggctcctcat ggcccggctc cttagcacct ctccagctct 180  
 tcaggggaaca ccagcatccc gaggggttctt cgcagctgcc atcctcttcc tatcacagtc 240  
 ccacgtggcg cggggccacc cgggctcaga ccaggcagtg ctagccctgt cccctgagta 300  
 tgagggcatc tggggcgacc tgcaggagct ctggttcctg ggcattcaag ccttcaccgg 360  
 ctgtgtgcct ctgctgc 377

<210> 37  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (96)

<400> 37  
 Met Asn Thr Leu Met Thr Ser Leu Pro Ala Leu Val Gln Gln Gln Gly  
 1 5 10 15  
 Arg Leu Leu Leu Ala Ala Asn Val Ala Thr Leu Gly Leu Leu Met Ala  
 20 25 30  
 Arg Leu Leu Ser Thr Ser Pro Ala Leu Gln Gly Thr Pro Ala Ser Arg  
 35 40 45  
 Gly Phe Phe Ala Ala Ala Ile Leu Phe Leu Ser Gln Ser His Val Ala  
 50 55 60  
 Arg Ala Thr Pro Gly Ser Asp Gln Ala Val Leu Ala Leu Ser Pro Glu  
 65 70 75 80  
 Tyr Glu Gly Ile Trp Ala Asp Leu Gln Glu Leu Trp Phe Leu Gly Xaa  
 85 90 95  
 Gln Ala Phe Thr Gly Cys Val Pro Leu Leu  
 100 105

<210> 38  
 <211> 245

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (3)

<220>  
<221> unsure  
<222> (17)

<220>  
<221> unsure  
<222> (34)

<220>  
<221> unsure  
<222> (46)

<220>  
<221> unsure  
<222> (65)

<220>  
<221> unsure  
<222> (71)

<220>  
<221> unsure  
<222> (142)

<220>  
<221> unsure  
<222> (214)

<400> 38  
tangactcct ctctgcngag acgcgactgg cggntccagc agggantacc ttttttataa 60  
accnnggggg nccacacaca cacacacaca cacacacaca cacacacaca 120  
catttttgat cccttgcttc cntcccccag tgcgttctgt gatcgccaag ttcaaagctg 180  
tgcacatgtg gacactcaat aaatgttcat tggngacaaa aaaaaaaaaa aaaaaaaaaa 240  
aaaaa 245

<210> 39  
<211> 2384  
<212> DNA  
<213> Homo sapiens

<400> 39  
ccaaaacatg ctcaaaagta gaacattttg tttcaatatt aggaaagtgc tttgaatccc 60  
cttggacgac aaaagcgttg tctgagacag catgcgaaga ctcagaggaa aacaagcaga 120  
gaataacagg tgcccagact ctaccaaagc atgtttctac cagcagtgat gaagggagcc 180  
ccagtgccag tacaccaatg atcaataaaa ctggccttaa attttcagct gagaagcctg 240  
tgattgaagt tcccagcatg acaatcctgg ataaaaagga tggagagcag gccaaagccc 300  
tgtttgagaa agtgaggaag ttccgtgccc atgtggaaga tagtgacttg atctataaac 360  
tctatgtggt ccaaacagtt atcaaaacag ccaagtccat ttttattctc tgctatacag 420  
cgaactttgt caacgcaatc agctttgaac acgtctgcaa gcccaaagtt gagcatctga 480  
ttggttatga ggtatttgag tgcaccaca atatggctta catgttgaaa aagcttctca 540  
tcagttacat atccattatt tgtgtttatg gctttatctg cctctacact ctcttctggt 600  
tattcaggat acctttgaag gaatattctt tcgaaaaagt cagagaagag agcagtttta 660  
gtgacattcc agatgtcaaa aacgattttg cgttccttct tcacatggta gaccagtatg 720

accagctata ttccaagcgt tttgggtgtgt tcttgtcaga agttagttaa aataaactta 780  
 gggaaattag tttgaacccat gagggtgacat ttgaaaaact caggcagcac atttcacgca 840  
 acgcccagga caagcaggag ttgcatctgt tcatgtctgtc ggggggtgccc gatgctgtct 900  
 ttgacctcac agacctgact aacctccaag agctccacct ctgccactgc cctgcaaaag 960  
 ctaagatttc tcaaatgact aacctccaag agctccacct ctgccactgc cctgcaaaag 1020  
 ttgaacagac tgccttttagc tttcttcgcg atcacttgag atgccttcac gtgaagttca 1080  
 ctgatgtggc tgaaattcct gcctgggtgt atttgcctca aaaccttcga gaggttgtact 1140  
 taataggcaa tttgaactct gaaaacaata agatgatagg acttgaatct ctccgagagt 1200  
 tgcggcacct taagattctc cacgtgaaga gcaatttgac caaagttccc tccaacatta 1260  
 cagatgtggc tccacatctt acaaagttag tcattcataa tgacggcact aaactcttgg 1320  
 tactgaacag ccttaagaaa atgatgaatg tcgctgagct ggaactccag aactgtgagc 1380  
 tagagagaat cccacatgct attttcagcc tctctaattt acaggaactg gatttaagt 1440  
 ccaataacat tcgcacaatt gaggaaatca tcagtttcca gcatttaaaa cgactgactt 1500  
 gtttaaaatt atggcataac aaaattgtta ctattcctcc ctctattacc catgtcaaaa 1560  
 acttgagtc actttatttc tctaacaaca agctcgaatc cttaccagtg gcagtattta 1620  
 gtttacagaa actcagatgc ttagatgtga gctacaacaa catttcaatg attccaatag 1680  
 aaataggatt gcttcagaac ctgcagcatt tgcataatcag tgggaacaaa gtggacattc 1740  
 tgccaaaaca attgtttaaa tgcataaagt tgaggacttt gaactctggga cagaactgca 1800  
 tcacctcact cccagagaaa gttgggtcagc tctcccagct cactcagctg gagctgaagg 1860  
 ggaactgctt ggaccgcctg ccagcccagc tgggcccagt tgggatgctc aagaaaagcg 1920  
 ggcttgttgt ggaagatcac ctttttgata ccttgccact cgaagtcaaa gaggcattga 1980  
 atcaagacat aaatattccc tttgcaaatg ggatttamac taagataata tatgcacagt 2040  
 gatgtgcagg aacaacttcc tagattgcaa gtgctcagct acaagttatt acaagataat 2100  
 gcatttttagg agtagataca tcttttaaaa taaaacagag aggatgcata gaaggtctgat 2160  
 agaagacata actgaatggt caatgtttgt aggggttttaa gtcattcatt tccaaatcat 2220  
 tttttttttt cttttgggga aagggaagga aaaattataa tcaactaatct tggttctttt 2280  
 taaattgttt gtaacttggg tgcctgccgt actgaatggt tacaattatgc ttgcctgcta 2340  
 aagtaaatga ttaaatggac attttcttac tataaaaaaa aaaa 2384

&lt;210&gt; 40

&lt;211&gt; 614

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (607)

&lt;400&gt; 40

Met Ile Asn Lys Thr Gly Phe Lys Phe Ser Ala Glu Lys Pro Val Ile  
 1 5 10 15

Glu Val Pro Ser Met Thr Ile Leu Asp Lys Lys Asp Gly Glu Gln Ala  
 20 25 30

Lys Ala Leu Phe Glu Lys Val Arg Lys Phe Arg Ala His Val Glu Asp  
 35 40 45

Ser Asp Leu Ile Tyr Lys Leu Tyr Val Val Gln Thr Val Ile Lys Thr  
 50 55 60

Ala Lys Phe Ile Phe Ile Leu Cys Tyr Thr Ala Asn Phe Val Asn Ala  
 65 70 75 80

Ile Ser Phe Glu His Val Cys Lys Pro Lys Val Glu His Leu Ile Gly  
 85 90 95

Tyr Glu Val Phe Glu Cys Thr His Asn Met Ala Tyr Met Leu Lys Lys  
 100 105 110

Leu Leu Ile Ser Tyr Ile Ser Ile Ile Cys Val Tyr Gly Phe Ile Cys  
 115 120 125  
 Leu Tyr Thr Leu Phe Trp Leu Phe Arg Ile Pro Leu Lys Glu Tyr Ser  
 130 135 140  
 Phe Glu Lys Val Arg Glu Ser Ser Phe Ser Asp Ile Pro Asp Val  
 145 150 155 160  
 Lys Asn Asp Phe Ala Phe Leu Leu His Met Val Asp Gln Tyr Asp Gln  
 165 170 175  
 Leu Tyr Ser Lys Arg Phe Gly Val Phe Leu Ser Glu Val Ser Glu Asn  
 180 185 190  
 Lys Leu Arg Glu Ile Ser Leu Asn His Glu Trp Thr Phe Glu Lys Leu  
 195 200 205  
 Arg Gln His Ile Ser Arg Asn Ala Gln Asp Lys Gln Glu Leu His Leu  
 210 215 220  
 Phe Met Leu Ser Gly Val Pro Asp Ala Val Phe Asp Leu Thr Asp Leu  
 225 230 235 240  
 Asp Val Leu Lys Leu Glu Leu Ile Pro Glu Ala Lys Ile Pro Ala Lys  
 245 250 255  
 Ile Ser Gln Met Thr Asn Leu Gln Glu Leu His Leu Cys His Cys Pro  
 260 265 270  
 Ala Lys Val Glu Gln Thr Ala Phe Ser Phe Leu Arg Asp His Leu Arg  
 275 280 285  
 Cys Leu His Val Lys Phe Thr Asp Val Ala Glu Ile Pro Ala Trp Val  
 290 295 300  
 Tyr Leu Leu Lys Asn Leu Arg Glu Leu Tyr Leu Ile Gly Asn Leu Asn  
 305 310 315 320  
 Ser Glu Asn Asn Lys Met Ile Gly Leu Glu Ser Leu Arg Glu Leu Arg  
 325 330 335  
 His Leu Lys Ile Leu His Val Lys Ser Asn Leu Thr Lys Val Pro Ser  
 340 345 350  
 Asn Ile Thr Asp Val Ala Pro His Leu Thr Lys Leu Val Ile His Asn  
 355 360 365  
 Asp Gly Thr Lys Leu Leu Val Leu Asn Ser Leu Lys Lys Met Met Asn  
 370 375 380  
 Val Ala Glu Leu Glu Leu Gln Asn Cys Glu Leu Glu Arg Ile Pro His  
 385 390 395 400  
 Ala Ile Phe Ser Leu Ser Asn Leu Gln Glu Leu Asp Leu Lys Ser Asn  
 405 410 415  
 Asn Ile Arg Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu Lys Arg  
 420 425 430

Leu Thr Cys Leu Lys Leu Trp His Asn Lys Ile Val Thr Ile Pro Pro  
 435 440 445  
 Ser Ile Thr His Val Lys Asn Leu Glu Ser Leu Tyr Phe Ser Asn Asn  
 450 455 460  
 Lys Leu Glu Ser Leu Pro Val Ala Val Phe Ser Leu Gln Lys Leu Arg  
 465 470 475 480  
 Cys Leu Asp Val Ser Tyr Asn Asn Ile Ser Met Ile Pro Ile Glu Ile  
 485 490 495  
 Gly Leu Leu Gln Asn Leu Gln His Leu His Ile Thr Gly Asn Lys Val  
 500 505 510  
 Asp Ile Leu Pro Lys Gln Leu Phe Lys Cys Ile Lys Leu Arg Thr Leu  
 515 520 525  
 Asn Leu Gly Gln Asn Cys Ile Thr Ser Leu Pro Glu Lys Val Gly Gln  
 530 535 540  
 Leu Ser Gln Leu Thr Gln Leu Glu Leu Lys Gly Asn Cys Leu Asp Arg  
 545 550 555 560  
 Leu Pro Ala Gln Leu Gly Gln Cys Arg Met Leu Lys Lys Ser Gly Leu  
 565 570 575  
 Val Val Glu Asp His Leu Phe Asp Thr Leu Pro Leu Glu Val Lys Glu  
 580 585 590  
 Ala Leu Asn Gln Asp Ile Asn Ile Pro Phe Ala Asn Gly Ile Xaa Thr  
 595 600 605  
 Lys Ile Ile Tyr Ala Gln  
 610

<210> 41  
 <211> 2386  
 <212> DNA  
 <213> Homo sapiens

<400> 41  
 ccaaaacatc aaaccctttt cttgtagcag cacaggattc tgagacagat tatgtcacia 60  
 cagataatct aacaaagggt actgaggaag tcgtggcaaa catgcctgaa ggcctgactc 120  
 cagatttagt acaggaagca tgtgaaagt aattgaatga agttactggt acaaagattg 180  
 cttatgaaac aaaaatggac ttggttcaaa catcagaagt tatgcaagag tcaactctatc 240  
 ctgcagcaca gctttgcccc tcatttgaag agtcagaagc tactccttca ccagttttgc 300  
 ctgacattgt tatggaagca ccattgaatt ctgcagttcc tagtctggt gcttccgtga 360  
 tacagcccag ctcatcacca ttagaagctt cttcagttta ttatgaaagc ataaaacatg 420  
 agcctgaaaa cccccacca tatgaagagg ccatgagtgt atcactaaaa aaagtatcag 480  
 gaataaagga agaaattaaa gagcctgaaa atattaatgc agctcttcaa gaaacagaag 540  
 ctcccttat atctaattgca tgtgatttaa ttaagaaac aaagctttct gctgaaccag 600  
 ctccggattt ctctgattat tcagaaatgg caaaagtga acagccagt cctgatcatt 660  
 ctgagctagt tgaagattcc tcacctgatt ctgaaccagt tgacttattt agtgatgatt 720  
 caatacctga cgttccacaa aaacaagatg aaactgtgat gcttggtgaa gaaagtctca 780  
 ctgagacttc atttgagtca atgatagaat atgaaaataa ggaaaaactc agtgctttgc 840  
 cacctgaggg aggaaagcca tatttggaat cttttaagct cagtttagat aacacaaaag 900  
 ataccctgtt acctgatgaa gtttcaacat tgagcaaaaa ggagaaaatt cctttgcaga 960  
 tggaggagct cagtactgca gtttattcaa atgatgactt atttatttct aaggaagcac 1020



agataagaga aactgaaacg ttttcagatt catctccaat tgaaattata gatgagttcc 1080  
 ctacattgat cagttctaaa actgattcat tttctaaatt agccagggaa tatactgacc 1140  
 tagaagtcac ccacaaaagt gaaattgcta atgccccgga tggagctggg tcattgcctt 1200  
 gcacagaatt gccccatgac ctttctttga agaacatata acccaaagtt gaagagaaaa 1260  
 tcagtttttc agatgacttt tctaaaaaat ggtctgtac atcaaaggtg ctcttattgc 1320  
 ctccagatgt ttctgctttg gccactcaag cagagataga gagcatagtt aaacccaaag 1380  
 ttcttggtga agaagctgag aaaaaacttc cttccgatac agaaaaagag gacagatcac 1440  
 catctgctat attttcagca gagctgagta aaacttcagt tgttgacctc ctgtactgga 1500  
 gagacattaa gaagactgga gtggtgtttg gtgccagcct attcctgctg ctttcattga 1560  
 cagtattcag cattgtgagc gtaacagcct acattgcctt ggccctgctc tctgtgacca 1620  
 tcagcttttag gatatacaag ggtgtgatcc aagctatcca gaaatcagat gaaggccacc 1680  
 cattcagggg agttgctata tctgaggagt tgggttcagaa gtacagtaat tctgctcttg 1740  
 gtcatgtgaa ctgcacgata aaggaactca ggcgcctctt cttagttagt gatttagttg 1800  
 attctctgaa gtttgtagtg ttgatgtggg tatttaccta tgttggtgcc ttgtttaatg 1860  
 gtctgacact actgattttg gctctcattt cactcttcag tgttctctgt atttatgaac 1920  
 ggcacagggc acagatagat cattatctag gacttgcaaa taagaatgtt aaagatgcta 1980  
 tggctaaaaat ccaagcaaaa atccctggat tgaagcgcaa agctgaatga aaacgcccac 2040  
 aataattagt aggagtcat ctttaaaggg gatattcatt tgattatacg ggggaggggc 2100  
 agggagaagac gaaccttgac gttgcagtc agtttcacag atcgttgta gatctttatt 2160  
 ttagccatg cactgttggt agggaaaaat acctgtctt actgccatgt gttcatcatc 2220  
 ttaagtattg taagctgcta tgtatggatt taaaccgtaa tcatatcttt ttcctatctg 2280  
 aggcactggg ggaataaaaa acctgtatat ttactttgt tgcagatagt cttgccgcac 2340  
 cttggcaagt tgcagagatg gtggagctag aaaaaaaaaa aaaaaa 2386

&lt;210&gt; 42

&lt;211&gt; 642

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser  
 1 5 10 15  
 Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met  
 20 25 30  
 Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro Ala  
 35 40 45  
 Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro  
 50 55 60  
 Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val Pro  
 65 70 75 80  
 Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala  
 85 90 95  
 Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro  
 100 105 110  
 Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly Ile  
 115 120 125  
 Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu  
 130 135 140  
 Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr  
 145 150 155 160

Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met  
 165 170 175  
 Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu Asp  
 180 185 190  
 Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile  
 195 200 205  
 Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys Glu  
 210 215 220  
 Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn Lys  
 225 230 235 240  
 Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu Glu  
 245 250 255  
 Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro Asp  
 260 265 270  
 Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met Glu  
 275 280 285  
 Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser Lys  
 290 295 300  
 Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro Ile  
 305 310 315 320  
 Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp Ser  
 325 330 335  
 Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His Lys  
 340 345 350  
 Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys Thr  
 355 360 365  
 Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val Glu  
 370 375 380  
 Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala Thr  
 385 390 395 400  
 Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr Gln  
 405 410 415  
 Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu Ala  
 420 425 430  
 Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro Ser  
 435 440 445  
 Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu Leu  
 450 455 460  
 Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu  
 465 470 475 480

Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala  
 485 490 495  
 Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr  
 500 505 510  
 Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe  
 515 520 525  
 Arg Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser  
 530 535 540  
 Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe  
 545 550 555 560  
 Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp  
 565 570 575  
 Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile  
 580 585 590  
 Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His  
 595 600 605  
 Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val Lys  
 610 615 620  
 Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys  
 625 630 635 640  
 Ala Glu

<210> 43  
 <211> 344  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (13)

<220>  
 <221> unsure  
 <222> (39)

<220>  
 <221> unsure  
 <222> (185)

<220>  
 <221> unsure  
 <222> (260)

<400> 43  
 ggccgctgcg ganccggcgg tccttgcgct ccccaacanc ggccgcccgg ggcggggggc 60  
 gccgtcgggc acagtcgccg tgctctctcg ttcttcagtc ttccgcgcgac cctcgtcggc 120  
 gccacacggg gcgggctaca agctgctcat ccagaagttc ctcagcctgt acggcgacca 180  
 gatcnacatg caccgcaaat tcgtggtgca gctgttcgcc gaggagtggg gccagtacgt 240

ggacttgccc aagggtcttcn cgggtgagcga gcgctgcaag gtgcgcctcg tgccgctgca 300  
tatccagctc actaccctgg gaaatcttac accttcaagc actg 344

<210> 44  
<211> 631  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (73)

<220>  
<221> unsure  
<222> (369)

<400> 44  
acatgattca gagtcctgtg ggtaaattca tatgcaataa tcttattcca atcaatctgt 60  
aaagtaaaag cantacatcc acattaacat tataacatct tacagtaata taaaagccaa 120  
atcattgttg gtacgtcatt ttctttaaag tgaacaattt aagaaaactt cacaagagtc 180  
tgcacttttg aaagatacga tcagagtaca cagtagagac aaaacaggca tcttcattgt 240  
aatttttttt aataaataaa agcacattaa caaaaaagga aggtaagcag caccggaagc 300  
ctttgacgtt tgtaactaaa tgctgggtact caattgaatc gagctgggta agtttacta 360  
ggagggcgna aaaaggagcc gtttttgact taacatttta attctagtag agataagaag 420  
agcttggttg ggcttacagt ccttcacctg actgtccttc accagttagt agcataccag 480  
ttcttcaaat gtcttatact ttggaaagca gacccgactc tggagcactc gccttaatta 540  
gattctgaat ttcttgaat tttggatggc ccttatcagc taccagctga agcagaacag 600  
cctcactcgt ggtcactatg atccccgttc g 631

<210> 45  
<211> 22  
<212> PRT  
<213> Homo sapiens

<400> 45  
Met Val Leu Ile Ser Tyr Gln Leu Lys Gln Asn Ser Leu Thr Arg Gly  
1 5 10 15  
His Tyr Asp Pro Gly Ser  
20

<210> 46  
<211> 70  
<212> DNA  
<213> Homo sapiens

<400> 46  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60  
aaaaaaaaaa 70

<210> 47  
<211> 428  
<212> DNA  
<213> Homo sapiens

<400> 47  
agcacgcggt cctgcccgtg gacggggcaa cgctggcaga tgtgatgcgc cagcggggca 60  
tcaacatgcg ctacctgggc aagggtgctg agctgggtgct gcggarcccg gcccgccacc 120  
agctggacca cgtctttaa atcggcattg gagaactcat caccgctcg sccaagcaca 180

tcttcaagac gtacttacag ggagtcgagc tctccggcct ctcagccgcc atcagccact 240  
 tcctgaactg cttcctgagc tcctacccaa acccctgtggc ccacctgccc gccgacgagc 300  
 tggctctcaa gaagcggaat aagaggagga aaaaccggcc cccgggggct gcagataaca 360  
 cagcctgggc tgcctgacc ccccaggagc tctggaagaa catctgccag gaggccaaga 420  
 actacttt 428

<210> 48  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (21)

<220>  
 <221> UNSURE  
 <222> (43)

<400> 48  
 Met Arg Gln Arg Gly Ile Asn Met Arg Tyr Leu Gly Lys Val Leu Glu  
 1 5 10 15  
 Leu Val Leu Arg Xaa Pro Ala Arg His Gln Leu Asp His Val Phe Lys  
 20 25 30  
 Ile Gly Ile Gly Glu Leu Ile Thr Arg Ser Xaa Lys His Ile Phe Lys  
 35 40 45  
 Thr Tyr Leu Gln Gly Val Glu Leu Ser Gly Leu Ser Ala Ala Ile Ser  
 50 55 60  
 His Phe Leu Asn Cys Phe Leu Ser Ser Tyr Pro Asn Pro Val Ala His  
 65 70 75 80  
 Leu Pro Ala Asp Glu Leu Val Ser Lys Lys Arg Asn Lys Arg Arg Lys  
 85 90 95  
 Asn Arg Pro Pro Gly Ala Ala Asp Asn Thr Ala Trp Ala Val Met Thr  
 100 105 110  
 Pro Gln Glu Leu Trp Lys Asn Ile Cys Gln Glu Ala Lys Asn Tyr Phe  
 115 120 125

<210> 49  
 <211> 245  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (46)

<220>  
 <221> unsure  
 <222> (138)

<220>  
 <221> unsure

&lt;222&gt; (147)

&lt;400&gt; 49

tgggtggggga ggatgtgccc accctgagac cgggaggaga cgggcntttg cctgggtttg 60  
 cggagagccg cttatgggtg tgggtccgtcc agacaccttg tttcaagggg gatgggcgtg 120  
 agcgggcaag cagagcancc ccaccgntga gcaagaactt ttttttggtt ttaaaccatc 180  
 acgtcctcat ttcacattgg aataaagtga gtttttgaaa aaaaaaaaaa aaaaaaaaaa 240  
 aaaaaa 245

&lt;210&gt; 50

&lt;211&gt; 566

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

cagtgaagccc tttgaaaaat aaacatccag atgaagatgc tgtggaagct gaggggcatg 60  
 aggtaaaaag actcagggtt gacaaagaag gtgaagtcag agaaacagcc agtcaaacga 120  
 cttccagcga aatttcttca gttatggtag gagaacaga agcatcatct tcatctcagg 180  
 ataaagacaa agatagccgt tgtwcccgcc agcactgtwc agaagaggat gaagaagagg 240  
 atgaagagga agaagaagag tcttttatga catcaagaga aatgatccca gaaagaaaaa 300  
 atcaagaaaa agaattctgat gatgccttaa ctgtgaaatga agagacttct gaggaaaaata 360  
 atcaaatgga ggaattctgat gtgtctcaag ctgagaaaga tttgctacat tctgaaggta 420  
 gtgaaaacga aggccctgta agtagtagtt cttctgactg ccgtgaaaca gaagaattag 480  
 taggatccaa ttccagtaaa actggagaga ttctttcaga atcatccatg gaaaatgatg 540  
 acgaagccac agaagtcacc gatgaa 566

&lt;210&gt; 51

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (21)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (26)

&lt;400&gt; 51

Met Val Gly Glu Thr Glu Ala Ser Ser Ser Ser Gln Asp Lys Asp Lys  
 1 5 10 15  
 Asp Ser Arg Cys Xaa Arg Gln His Cys Xaa Glu Glu Asp Glu Glu Glu  
 20 25 30  
 Asp Glu Glu Glu Glu Glu Ser Phe Met Thr Ser Arg Glu Met Ile  
 35 40 45  
 Pro Glu Arg Lys Asn Gln Glu Lys Glu Ser Asp Asp Ala Leu Thr Val  
 50 55 60  
 Asn Glu Glu Thr Ser Glu Glu Asn Asn Gln Met Glu Glu Ser Asp Val  
 65 70 75 80  
 Ser Gln Ala Glu Lys Asp Leu Leu His Ser Glu Gly Ser Glu Asn Glu  
 85 90 95  
 Gly Pro Val Ser Ser Ser Ser Ser Asp Cys Arg Glu Thr Glu Glu Leu  
 100 105 110

Val Gly Ser Asn Ser Ser Lys Thr Gly Glu Ile Leu Ser Glu Ser Ser  
 115 120 125

Met Glu Asn Asp Asp Glu Ala Thr Glu Val Thr Asp Glu  
 130 135 140

<210> 52  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 52  
 tcatcatggc tataaatacc aaaacgattt ggatccattt atgtttgtag gataatatac 60  
 tactgactga cttgactgtc aggttcacaa cagctagatg atatatattat gactatgtct 120  
 aatagttgaa ataaaatctg aatattgatt tactataccc aagaggggag aaaaattaac 180  
 cattgtaaat ttttaaaaat tttttcaaaa atgttataat gaggcataat taagtttaca 240  
 aattttgaaa ttttcttttg aatattttatg aaattgtcag taaacttacc taagatcctg 300  
 tgaccttttg atatttttta ttttaattgt agtgccatgg accattttgt aacaaattga 360  
 tttacttttg ttggttgtaa gttgaagatt tagcattatg actttgaggt ctgtgggttt 420  
 atttgtaaac ttgcaattgc tatatttgca agggcaaatg tatttcttta ttaataaaag 480  
 tacaataatg gtgaatgtac caaatgaca tcacttataa aaaaaaaaaa a 531

<210> 53  
 <211> 1163  
 <212> DNA  
 <213> Homo sapiens

<400> 53  
 kctggaacca cgcggargaa ggaagagacg caggcaggct gcggttacc aagcggscac 60  
 ccgggcctca gggacccttc cccgagagac ggcaccatga cccagggaaa gctctccgtg 120  
 gctaacaagc ccctgggacc gaggggcagc agcakgtgca tggcgagaag aaggagctcc 180  
 agcagtgcgc tcagcccccac cctcctatga ggaaccacct ctggggaggg gatgaaggca 240  
 ggggccttcc cccagcccc caccagcggtg cctctccacc ctactggggc ctatgtggac 300  
 cccagcagca gctccagcta tgacaacggt ttccccaccg gagaccatga gctcttcacc 360  
 actttcagct gggatgacca gaaagtctgt cgagtctttg tcagaaagggt ctacaccatc 420  
 ctgctgattc agctgctggt gaccttggtt gctgtggctc tctttacttt ctgtgacctt 480  
 gtcaaggact atgtccaggc caaccaggc tgggtactggg catcctatgc tgtgttcttt 540  
 gcaacctacc tgaccttggt ttgctgttct ggaccaggga ggcatttccc ctggaacctg 600  
 atttctctga ccgtctttac cctgtccatg gcctacctca ctgggatgct gtccagctac 660  
 tacaacacca cctccgtgct gctgtgcctg ggcacacagg cccttgctg cctctcagtc 720  
 accgtcttca gcttccagac caagtccgac ttcacctcct gccagggcgt gctcttcgtg 780  
 ctctctcatg ctcttttctt cagcggactc atcctggcca tcctcctacc cttccaatat 840  
 gtgccctggc tccatgcagt ttatgcagca ctgggagcgg gtgtatttac attgttccctg 900  
 gcacttgaca cccagttgct gatgggtaac cgacgccact cgctgagccc tgaggagtat 960  
 atttttggag ccttcaacat ttacctagac atcatctata tcttcacctt cttcctgcag 1020  
 ctttttggca ctaaccgaga atgaggagcc ctccctgccc caccgtcctc cagagaatgc 1080  
 gccctcctg gtccctctgc cctcccctgc gctcctgcga gaccagatat aaaactagct 1140  
 gccaacccaa aaaaaaaaaa aaa 1163

<210> 54  
 <211> 270  
 <212> PRT  
 <213> Homo sapiens

<400> 54  
 Met Lys Ala Gly Ala Phe Pro Pro Ala Pro Thr Ala Val Pro Leu His  
 1 5 10 15

Pro Ser Trp Ala Tyr Val Asp Pro Ser Ser Ser Ser Tyr Asp Asn  
           20                          25                          30  
 Gly Phe Pro Thr Gly Asp His Glu Leu Phe Thr Thr Phe Ser Trp Asp  
           35                          40                          45  
 Asp Gln Lys Val Arg Arg Val Phe Val Arg Lys Val Tyr Thr Ile Leu  
           50                          55                          60  
 Leu Ile Gln Leu Leu Val Thr Leu Ala Val Val Ala Leu Phe Thr Phe  
           65                          70                          75                          80  
 Cys Asp Pro Val Lys Asp Tyr Val Gln Ala Asn Pro Gly Trp Tyr Trp  
                           85                          90                          95  
 Ala Ser Tyr Ala Val Phe Phe Ala Thr Tyr Leu Thr Leu Ala Cys Cys  
                           100                          105                          110  
 Ser Gly Pro Arg Arg His Phe Pro Trp Asn Leu Ile Leu Leu Thr Val  
           115                          120                          125  
 Phe Thr Leu Ser Met Ala Tyr Leu Thr Gly Met Leu Ser Ser Tyr Tyr  
           130                          135                          140  
 Asn Thr Thr Ser Val Leu Leu Cys Leu Gly Ile Thr Ala Leu Val Cys  
           145                          150                          155                          160  
 Leu Ser Val Thr Val Phe Ser Phe Gln Thr Lys Phe Asp Phe Thr Ser  
                           165                          170                          175  
 Cys Gln Gly Val Leu Phe Val Leu Leu Met Thr Leu Phe Phe Ser Gly  
           180                          185                          190  
 Leu Ile Leu Ala Ile Leu Leu Pro Phe Gln Tyr Val Pro Trp Leu His  
           195                          200                          205  
 Ala Val Tyr Ala Ala Leu Gly Ala Gly Val Phe Thr Leu Phe Leu Ala  
           210                          215                          220  
 Leu Asp Thr Gln Leu Leu Met Gly Asn Arg Arg His Ser Leu Ser Pro  
           225                          230                          235                          240  
 Glu Glu Tyr Ile Phe Gly Ala Leu Asn Ile Tyr Leu Asp Ile Ile Tyr  
                           245                          250                          255  
 Ile Phe Thr Phe Phe Leu Gln Leu Phe Gly Thr Asn Arg Glu  
           260                          265                          270

&lt;210&gt; 55

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (123)

&lt;400&gt; 55

cgcaccccct cgggcgcggg gcgcacgcggg ggcgctggtg gaktctgmga gggccasgtc 60



cggcgggcg ggcggcggt ggcactggct cgggactctg cccggccag ggcggcgmtc 120  
 canccgggag ggcgacgtgg agcgccack tggakcggcc cggggggargc tggcgggcg 180  
 akgcgaggcg cggcgggcgc akcakccakg agcgccacg gagstggacc cccagakccg 240  
 cgcggcgccg cagcagttcc aggaaggatg ttacctttga cgatgacagt gttaatcctg 300  
 ctgctgctcc ccacgggtca ggctgcccc aaggatggag tcacaaggcc agaactctga 360  
 gtgcagcatc agctcctgcc caacccttc cagccaggcc aggagcagct cggacttctg 420  
 cagagctacc taaagggact aggaaggaca gaagtgaac tggagcatct gagccgggag 480  
 caggttctcc tctacctctt tgcctccat gactatgacc agagtggaca gctggatggc 540  
 ctggagctgc tgtccatgtt gacagctgct ctggccctg gagctgcca ctctctacc 600  
 accaaccggt tgatcttgat agtg 624

<210> 56

<211> 119

<212> PRT

<213> Homo sapiens

<400> 56

Met Leu Pro Leu Thr Met Thr Val Leu Ile Leu Leu Leu Leu Pro Thr  
 1 5 10 15

Gly Gln Ala Ala Pro Lys Asp Gly Val Thr Arg Pro Glu Ser Glu Val  
 20 25 30

Gln His Gln Leu Leu Pro Asn Pro Phe Gln Pro Gly Gln Glu Gln Leu  
 35 40 45

Gly Leu Leu Gln Ser Tyr Leu Lys Gly Leu Gly Arg Thr Glu Val Gln  
 50 55 60

Leu Glu His Leu Ser Arg Glu Gln Val Leu Leu Tyr Leu Phe Ala Leu  
 65 70 75 80

His Asp Tyr Asp Gln Ser Gly Gln Leu Asp Gly Leu Glu Leu Leu Ser  
 85 90 95

Met Leu Thr Ala Ala Leu Ala Pro Gly Ala Ala Asn Ser Pro Thr Thr  
 100 105 110

Asn Pro Val Ile Leu Ile Val  
 115

<210> 57

<211> 80

<212> DNA

<213> Homo sapiens

<400> 57

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60  
 aaaaaaaaaa aaaaaaaaaa 80

<210> 58

<211> 2160

<212> DNA

<213> Homo sapiens

<400> 58

agacagggaa tactttattc aaaaccatc acagaaatgg acagcttggg tctgtaacaa 60  
 agcattcatg ttttagagca taggtcagta attgtatatg agagcatata ctgctacata 120  
 caaattaact gatcagacca caacttttca atgttttaaa cagaataagc ttcctgtaa 180

aagcagcacc ttgtgacgt ttttaacttta gtatttctct ctttcttctt caccctctcc 240  
 ttcaacagaa tccacaccaa cctcctcata atccttctct gcagcacatg aatcacaggt 300  
 attcctactg caagcgggag gcgaggagc ggggaagcggc ggagcgcgag ggcgcgcgaga 360  
 aagggcactt ggaacccacc gagctgctga tgaaccgggc ttacttgcag agcattaccc 420  
 ctgaggggta ctctgactcg gaggagaggg agagtatgcc gagggatggc gagagcgcgaga 480  
 aggagcacga gaaagaaggc gaggatggct acgggaagct gggcagacag gatggcgcagc 540  
 aggagttcga ggaggaagag gaagaaagtg aaaataaaag tatggatacg gatcccgaaa 600  
 cgatacgaga tgaagaagag actggagatc actccatgga cgatagttcg gaggatggga 660  
 aaatggaaac caaatcagac cagcaggaag acaatatgga agatggcatg taataaacta 720  
 ctgcatttta agcttctctat ttttttttcc agtagtattg ttacctgctt gaaaacactg 780  
 ctgtgttaag ctgttctatg acgtgcctga cgcttccagg aagctgtaga gagggacaga 840  
 aggggcgggt cagccaagac agatgtagac ggagttggag ctgggtattg ttaaaaactg 900  
 cattatgcaa aaatttttga cagtgttaag gcctaaaaac tgtgtggttc agagactaat 960  
 tcctgtgttt aatagcattt atactttaag cacaactaga aaattgtaag aattgcactc 1020  
 tacttatgta tcaactacaaa ctttaaaaaa ctatgtctaa tttatattaa tacattttta 1080  
 aaagtgcccc gcactaccat acatcagtat ttttattatt attattgta ttccttttta 1140  
 atttaagtgt ctgcactac aatgcacag tattatgatt cctctgtact ttccttttgc 1200  
 tattcatcaa tttcccatct tttttttcag cttaagtaac cacacaattt taggctcaa 1260  
 tttttttttt tctgtgaagg aacttgaagt gatgcatgtg tgaatttaag ataccgaagt 1320  
 cttaagtgga cctggacgtg aaggaaaaag taagatgaga aataaagaaa gcctttgtaa 1380  
 ggtggtttta aaagccttat atgcaaacct ttaactctgt gtttctgcaa gtgccatcct 1440  
 tgtacagtgt taagagggta acatgggtta cctttgcacc agcttcagtg ttaagctcac 1500  
 cctgttcttt gaagcaccca tctcagttat agaagaatag gcagcagttc cttagtttac 1560  
 atatgtttgt gcaattattt tctgtacttt tttgttcatt aattttgtca gtattacacc 1620  
 aaactgtttt tgcaacaaaa aaattttttt tgcattcatt taatttttag tcaataaca 1680  
 ttttatttat gtggctcatt ttatatctcc taattttatt tatttcatac tgtagtgtac 1740  
 agtattatag ttcttcaata tatagatata ttttagtaaa aaaggaacat gacgttgatc 1800  
 atttgggcaa attttacgta aagagaagag catttattgt gttttggaac attaatgtg 1860  
 agatgggatt tttcaatttt attattttat ttttgttttt tccaattac tggaaattcc 1920  
 aaatttgga acttttgata cgatcttctg aaaacactgt attttcgact gaaaattcca 1980  
 ctttcttcat ctgttttttt agctaaaaag agggactgtt aaatacaatg tatgatacca 2040  
 tgacaaaaat ctttcttgaa ttgtctttgt aaaagtatta ttgaattttc aatttgtaat 2100  
 tctttttgaa aatgaccatg ctggaataaa aatgtagcca aactaaaaaa aaaaaaaaaa 2160

&lt;210&gt; 59

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

Met Asn His Arg Tyr Ser Tyr Cys Lys Arg Glu Ala Glu Glu Arg Glu  
 1 5 10 15

Ala Ala Glu Arg Glu Ala Arg Glu Lys Gly His Leu Glu Pro Thr Glu  
 20 25 30

Leu Leu Met Asn Arg Ala Tyr Leu Gln Ser Ile Thr Pro Gln Gly Tyr  
 35 40 45

Ser Asp Ser Glu Glu Arg Glu Ser Met Pro Arg Asp Gly Glu Ser Glu  
 50 55 60

Lys Glu His Glu Lys Glu Gly Glu Asp Gly Tyr Gly Lys Leu Gly Arg  
 65 70 75 80

Gln Asp Gly Asp Glu Glu Phe Glu Glu Glu Glu Glu Ser Glu Asn  
 85 90 95

Lys Ser Met Asp Thr Asp Pro Glu Thr Ile Arg Asp Glu Glu Glu Thr  
 100 105 110

Gly Asp His Ser Met Asp Asp Ser Ser Glu Asp Gly Lys Met Glu Thr  
 115 120 125

Lys Ser Asp His Glu Glu Asp Asn Met Glu Asp Gly Met  
 130 135 140

<210> 60  
 <211> 2168  
 <212> DNA  
 <213> Homo sapiens

<400> 60  
 gcagttactg ggagggggct tgctgtggcc ctgtcaggaa gagtagagct ctgggtccagc 60  
 tccgcgcagg gagggaggct gtcaccatgc cggcctgctg cagctgcagt gatgttttcc 120  
 agtatgagac gaacaaagtc actcggatcc agagcatgaa ttatggcacc attaatgtgt 180  
 tcttccacgt gatcatcttt tctcagcttc gctttgcttc ggtgagtgac aagctgtacc 240  
 agcggaaaaga gcctgtcatc agttctgtgc acaccaaggt gaaggggata gcagaggtga 300  
 aagaggagat cgtggagaat ggagtgaaga agttgggtgca cagtgtcttt gacaccgcag 360  
 actacacctt ccttttgcag gggaaactctt tcttcgtgat gacaaacttt ctcaaaacag 420  
 aaggccaaga gcagcgggtg tgtcccgagt atcccaccgc caggacgctc tgttcctctg 480  
 accgaggttg taaaaaggga tggatggacc cgagagcaa aggaattcag accggaaggt 540  
 gtgtagtga tgaagggaac cagaagacct gtgaagtctc tgcctgggtg cccatcgagg 600  
 cagtggaga gggcccccg cctgctctct tgaacagtgc cgaaaacttc actgtgtcga 660  
 tcaagaacaa tatcgacttc cccggccaca actacaccac gagaacatc ctgccagggt 720  
 caaacatcac ttgtaccttc cacaagactc agaattccca gtgtccatt ttcgcactag 780  
 gagacatctt ccgagaaaca ggcgataatt ttccagatgt ggcaattcag ggcggaataa 840  
 tgggcattga gatctactgg gactgcaacc tagaccgttg gtcccatcac tgcattccca 900  
 aatacagttt ccgtcgcttc gacgacaaga ccaccaacgc gtccttgtac cctgggtaca 960  
 acttcagata cgccaagtac tacaaggaaa acaatgttga gaaacgact ctgataaaaag 1020  
 tcttcgggat ccgttttgac atcctgggtt ttggcaccgg aggaaaattt gacattatcc 1080  
 agctgggtgt gtacatcggc tcaacctctt cctacttcgg tctggccgct gtgttcacgt 1140  
 acttccctcat cgacacttac tccagtaact gctgtcgttc ccatatttat ccttggtgca 1200  
 agtgctgtca gccctgtgtg gtcaacgaat actactacag gaagaagtgc gagtccattg 1260  
 tggagccaaa gccgacatta aagtatgtgt cctttgtgga tgaatccac attaggatgg 1320  
 tgaaccagca gctactaggg agaagtctgc aagatgtcaa gggccaagaa gtccaagac 1380  
 ctgcgatgga cttacagat ttgtccaggc tgccccctgc cctccatgac acacccccga 1440  
 ttcttgga accagaggag atacagctgc ttgaaaagga ggcgactcct agatccaggg 1500  
 atagccccgt ctggtgccag tgtggaagct gcctcccatc tcaactccct gagagccaca 1560  
 ggtgcctgga ggagctgtgc tgccggaaaa agccgggggc ctgcatcacc acctcagagc 1620  
 tgttcaggaa gctggtcctg tccagacacg tctgcagtt cctcctgtc taccaggagc 1680  
 ccttgctggc gctggatgtg gattccacca acagccggct gcggcactgt gcctacaggt 1740  
 gctacgccac ctggcgcttc ggctcccagg acatggctga ctttgccatc ctgcccagct 1800  
 gctgcccgtg gaggatcccg aaagagtctt cgaagagtga agggcagtac agtggcttca 1860  
 agagtcccta ctgaagccag gcgcccgtgc tcacgtctgt aatcccagcg ctttgggagg 1920  
 ccgaggcagg cagatcacct gaggtcgga gttggagacc cgcttggtca acaaggcgaa 1980  
 atcctgtctg tactaaaaat acaaaaatca gccagacatg gtggcatgca cctgcaatcc 2040  
 cagctactcg ggaggctgag gcacaagaat cacttgaacc cgggaggcag aggtttagt 2100  
 gagcccagat tgtgccactg ctctccagcc tgggaggcac agcaaaactgt ccccaaaaaa 2160  
 aaaaaaaa 2168

<210> 61  
 <211> 595  
 <212> PRT  
 <213> Homo sapiens

<400> 61  
 Met Pro Ala Cys Cys Ser Cys Ser Asp Val Phe Gln Tyr Glu Thr Asn  
 1 5 10 15

Lys Val Thr Arg Ile Gln Ser Met Asn Tyr Gly Thr Ile Lys Trp Phe  
 20 25 30  
 Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp  
 35 40 45  
 Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys  
 50 55 60  
 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val  
 65 70 75 80  
 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro  
 85 90 95  
 Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu  
 100 105 110  
 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu  
 115 120 125  
 Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser  
 130 135 140  
 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys  
 145 150 155 160  
 Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala  
 165 170 175  
 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile  
 180 185 190  
 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile  
 195 200 205  
 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro  
 210 215 220  
 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp  
 225 230 235 240  
 Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile  
 245 250 255  
 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys His Pro Lys  
 260 265 270  
 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr  
 275 280 285  
 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val  
 290 295 300  
 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu  
 305 310 315 320  
 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr  
 325 330 335

Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp  
 340 345 350  
 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr  
 355 360 365  
 Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr  
 370 375 380  
 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr  
 385 390 395 400  
 Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu  
 405 410 415  
 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro  
 420 425 430  
 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp  
 435 440 445  
 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys  
 450 455 460  
 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly  
 465 470 475 480  
 Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu  
 485 490 495  
 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu  
 500 505 510  
 Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu  
 515 520 525  
 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg  
 530 535 540  
 Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser  
 545 550 555 560  
 Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg  
 565 570 575  
 Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly Gln Tyr Ser Gly Phe Lys  
 580 585 590  
 Ser Pro Tyr  
 595

&lt;210&gt; 62

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

taaagatctg tggttcagagt cataactgaay agagacttct ggactctata gaaccactg 60

```

cctcctgatg aagtcacctac tgttcaccct tgcagttttt atgctcctgg cccaattggt 120
ctcaggtaat tggatgtga aaaagtgtct aaacgacgtt ggaatttgca agaagaagtg 180
caaacctgaa gagatgcatg taaagaatgg ttgggcaatg tgcggcaaac aaagggactg 240
ctgtgtttcca gctgacagac gtgctaatta tctgttttc tgtgtccaga caaagactac 300
aagaatttca acagtaacag caacaacagc aacaacaact ttgatgatga ctactgttc 360
gatgtcttcg atggctccta cccgtttctc ccactgggtg aacattccag cctctgtctc 420
ctgctctagg
430

```

<210> 63  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

```

<400> 63
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
 1             5             10            15
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
          20             25            30
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
          35             40            45
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
          50             55            60
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
          65             70            75            80
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
          85             90            95
Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu Asn
          100            105            110
Ile Pro Ala Ser Val Ser Cys Ser Arg
          115            120

```

<210> 64  
 <211> 112  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (8)

<220>  
 <221> unsure  
 <222> (12)

<220>  
 <221> unsure  
 <222> (36)

<220>  
 <221> unsure  
 <222> (41)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (44)

&lt;400&gt; 64

tttctctgntt tnggatcccc gattcattaa agcaangggg nttnaaaaaa aaaaaaaaaa 60  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 112

&lt;210&gt; 65

&lt;211&gt; 324

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (69)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (74)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (125)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (159)

&lt;400&gt; 65

nctaccccaa cctgtgtggc tggggccgagg tctccctca agggcctggg gccgtgcctc 60  
gggtgtacnc gtanggggtct gtgtgctggg ggtggctcac cgggcagcgt gggtagcgg 120  
cgcancggcg gcagcggaga acgagagagg ggagcagana cagaatcgcc taagctgaag 180  
tgtattggcg ccatcatggc tcaactgcggc ctccggctcc ttggctcggg tgattctcct 240  
gcctgagcct ccctagtagc taggactaca gtgctgtaga agaaaatcac atgattggtg 300  
ccctcaaaaa attggtgcca cttg 324

&lt;210&gt; 66

&lt;211&gt; 794

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (61)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (82)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (108)..(120)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (184)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (754)

&lt;400&gt; 66

cattatttca tcaccagaga atacacatgc agcaaatagc attgtgagtc aaactattcc 60  
 naaagcacag attcagcaat cnacacacac tcatctggat atctcacnnn nnnnnnnnnn 120  
 ttaactgatg aaaaaagtaa tggaacaatt gcccttgagg atgattctga ggatcctgga 180  
 gccnatgtat ctaacataca gcttcagcaa aaaatttcaa gtctggagat taaactcaaa 240  
 gtatctgaag aagaaaaaca gagaattaaa caggatgtgg aakcattgat ggaaaagcat 300  
 aatgtcttag aaaaaggcct tctaaaagaa aaagagcaag aggccatttc ttttcaagat 360  
 agatacaaa aacttcagga aaaacataaa caagaattgg aagacatgag gaaagctggt 420  
 cacgaagccc tcagcattat tgtggatgaa tataaggcac tactgcagtc ttcagttaag 480  
 caacaagtag aagctattga aaaacagtac atttctgcaa ttgagaaaca ggcacacaag 540  
 tgtgaggagt tgctaaatgc tcagcatcag aggctccttg aagtgtctaga tacagagaag 600  
 gaactgttaa aagaaaaaat aaaggaagct ttgattcagc aatctcaaga acagaaggaa 660  
 atattggaaa agtgttttga ggaagaaagg caaagaaata aagaggcatt agtatccgct 720  
 gcaaagcttg aaaaagaacc agtgaaggat gcantttttaa aattcgtaga agaagaaaga 780  
 aaaaaaaaaa aaaa 794

&lt;210&gt; 67

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (156)

&lt;400&gt; 67

Met Glu Lys His Asn Val Leu Glu Lys Gly Phe Leu Lys Glu Lys Glu  
 1 5 10 15  
 Gln Glu Ala Ile Ser Phe Gln Asp Arg Tyr Lys Glu Leu Gln Glu Lys  
 20 25 30  
 His Lys Gln Glu Leu Glu Asp Met Arg Lys Ala Gly His Glu Ala Leu  
 35 40 45  
 Ser Ile Ile Val Asp Glu Tyr Lys Ala Leu Leu Gln Ser Ser Val Lys  
 50 55 60  
 Gln Gln Val Glu Ala Ile Glu Lys Gln Tyr Ile Ser Ala Ile Glu Lys  
 65 70 75 80  
 Gln Ala His Lys Cys Glu Glu Leu Leu Asn Ala Gln His Gln Arg Leu  
 85 90 95  
 Leu Glu Val Leu Asp Thr Glu Lys Glu Leu Leu Lys Glu Lys Ile Lys  
 100 105 110  
 Glu Ala Leu Ile Gln Gln Ser Gln Glu Gln Lys Glu Ile Leu Glu Lys  
 115 120 125  
 Cys Leu Glu Glu Glu Arg Gln Arg Asn Lys Glu Ala Leu Val Ser Ala  
 130 135 140  
 Ala Lys Leu Glu Lys Glu Pro Val Lys Asp Ala Xaa Leu Lys Phe Val



145

150

155

160

Glu Glu Glu Arg

&lt;210&gt; 68

&lt;211&gt; 1494

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

```

cgtttgtcga cgccgctgcc accgcctgcc tgagagaagt cgctcgcgcc gaccccgctcg 60
cctccgcccgg ctaccatgtc cgcccaggcg cagatgcggg ccctgctgga ccagctcatg 120
ggcacggctc gggacggaga cgaaaccaga cagaggggtca agtttacaga tgaccgtgtc 180
tgcaagagtc accttctgga ctgctgcccc catgacatcc tggctgggac ggcgatggat 240
ttaggagaat gtacaaaaat ccacgacttg gccctccgag cagattatga gattgcaagt 300
aaagaaagag acctgttttt tgaattagat gcaatggatc acctggagtc ctttattgct 360
gaatgtgata ggagaactga gctcgccaag aagcggctgg cagaaacaca ggaggaaatc 420
agtgcggaag tttctgcaaa ggcaggaaaa gtacatgagt taaatgaaga aataggaaaa 480
ctccttgcta aagccgaaca gctaggggct gaaggtaatg tggatgaatc ccagaagatt 540
cttatggaag tggaaaaagt tcgtgcgaag aaaaaagaag ctgaggaaga atacagaaat 600
tccatgcctg catccagttt tcagcagcaa aagctgcgtg tctgcgaggt ctgttcagcc 660
taccttggtc tccatgacaa tgaccgtcgc ctggcagacc acttcggttg caagttacac 720
ttgggggttca ttcagatccg agagaagctt gatcagttga ggaaaactgt cgctgaaaag 780
caggagaaga gaaatcagga tcgcttgagg aggagagagg agagggaacg ggaggagcgt 840
ctgagcagga ggtcgggata aagaaccaga gatcgagga ggtcacgctc ccggggtcgg 900
cgctggaggc ggtcaagatc tacctcccga gagcgacgga aattgtcccc gtcgggtcc 960
cgagatagac atcgccgcca ccgcagccgt tcccggagcc acagccgggg acatcgctcg 1020
gcttcccggg accgaagtgc gaaatacaag taactactct gactccttcg gtagctgcaa 1080
ccaggagttc tccagagagc gggcatccag agaggagtcc tgggagagcg ggcggagcga 1140
cggagggccc ccggactgga ggccttgagc ctccaacggg aagatggctt cacggaggtc 1200
agaagagaag gggccggcg agatctgaac ccgtctcccg ggtgctgtaa atagtctgat 1260
aaacgttcac acagtctaaa attacccttt atatttgctg aatacaactc atcttttcta 1320
gtttaaaatt tctattgttt tggagctagc tgtgagtttc tagaagtgtc cagagttgct 1380
cctgtgttcc cgggtcatgt tgagtaggaa taaataaatc tgatgctgcc tcctggaaaa 1440
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1494

```

&lt;210&gt; 69

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

```

Met Ser Ala Gln Ala Gln Met Arg Ala Leu Leu Asp Gln Leu Met Gly
 1             5             10             15
Thr Ala Arg Asp Gly Asp Glu Thr Arg Gln Arg Val Lys Phe Thr Asp
 20             25             30
Asp Arg Val Cys Lys Ser His Leu Leu Asp Cys Cys Pro His Asp Ile
 35             40             45
Leu Ala Gly Thr Arg Met Asp Leu Gly Glu Cys Thr Lys Ile His Asp
 50             55             60
Leu Ala Leu Arg Ala Asp Tyr Glu Ile Ala Ser Lys Glu Arg Asp Leu
 65             70             75             80
Phe Phe Glu Leu Asp Ala Met Asp His Leu Glu Ser Phe Ile Ala Glu

```

85                                      90                                      95  
 Cys Asp Arg Arg Thr Glu Leu Ala Lys Lys Arg Leu Ala Glu Thr Gln  
    100                                      105                                      110  
 Glu Glu Ile Ser Ala Glu Val Ser Ala Lys Ala Gly Lys Val His Glu  
    115                                      120                                      125  
 Leu Asn Glu Glu Ile Gly Lys Leu Leu Ala Lys Ala Glu Gln Leu Gly  
    130                                      135                                      140  
 Ala Glu Gly Asn Val Asp Glu Ser Gln Lys Ile Leu Met Glu Val Glu  
    145                                      150                                      155                                      160  
 Lys Val Arg Ala Lys Lys Lys Glu Ala Glu Glu Glu Tyr Arg Asn Ser  
    165                                      170                                      175  
 Met Pro Ala Ser Ser Phe Gln Gln Gln Lys Leu Arg Val Cys Glu Val  
    180                                      185                                      190  
 Cys Ser Ala Tyr Leu Gly Leu His Asp Asn Asp Arg Arg Leu Ala Asp  
    195                                      200                                      205  
 His Phe Gly Gly Lys Leu His Leu Gly Phe Ile Gln Ile Arg Glu Lys  
    210                                      215                                      220  
 Leu Asp Gln Leu Arg Lys Thr Val Ala Glu Lys Gln Glu Lys Arg Asn  
    225                                      230                                      235                                      240  
 Gln Asp Arg Leu Arg Arg Arg Glu Glu Arg Glu Arg Glu Glu Arg Leu  
    245                                      250                                      255  
 Ser Arg Arg Ser Gly Ser Arg Thr Arg Asp Arg Arg Arg Ser Arg Ser  
    260                                      265                                      270  
 Arg Asp Arg Arg Arg Arg Arg Ser Arg Ser Thr Ser Arg Glu Arg Arg  
    275                                      280                                      285  
 Lys Leu Ser Arg Ser Arg Ser Arg Asp Arg His Arg Arg His Arg Ser  
    290                                      295                                      300  
 Arg Ser Arg Ser His Ser Arg Gly His Arg Arg Ala Ser Arg Asp Arg  
    305                                      310                                      315                                      320  
 Ser Ala Lys Tyr Lys  
    325

<210> 70  
 <211> 1761  
 <212> DNA  
 <213> Homo sapiens

<400> 70  
 caaggggaagt tctgaggggt gagaggttgc tcattcgctca gagcgtgctg cccaccctcc 60  
 acccctgcat ggcagaaact gtgcagggga cgaggccaag gaatcaggag acccagaggc 120  
 aggggtggcc cggagacggt gaagaaacca agacgcagag aggccaagcc ccttgcccttg 180  
 ggtcacacag ccaaaggagg cagagccaga actcacaacc agatccagag gcaacagggg 240  
 catggccacc tgggacgaaa aggcagtcac ccgcagggcc aaggtggctc ccgctgagag 300  
 gatgagcaag ttcttaaggc acttcacggt cgtgggagac gactaccatg cctggaacat 360

caactacaag aaatgggaga atgaagagga ggaggaggag gaggagcagc caccacccac 420  
 accagtctca ggcgaggaag gcagagctgc agcccttgac gttgcccctg cccctggccc 480  
 cgcacccagg gcccccttg acttcagggg catgttgagg aaactgttca gctcccacag 540  
 gtttcaggtc atcatcatct gcttgggtgt tctggatgcc ctctgggtgc ttgctgagct 600  
 catcctggac ctgaagatca tccagcccga caagaataac tatgctgcca tggatttcca 660  
 ctacatgagc atcaccatct tggctctttt tatgatggag atcatcttta aattatttgt 720  
 cttccgctg gagttctttc accacaagt tggatcctg gatgcccgtc tgggtggtgt 780  
 ctcatctac ctcgacattg tctcctgtt ccaggagcac cagtttgagg ctctgggcct 840  
 gctgattctg ctccggctgt ggcgggtggc ccggatcatc aatgggatta tcatctcagt 900  
 taagacacgt tcagaacggc aactcttaag gttaaaacag atgaatgtac aattggccgc 960  
 caagattcaa caccttgagt tcagctgctc tgagaaggaa caagaaattg aaagacttaa 1020  
 caaactattg cgacagcatg gacttcttgg tgaagtgaac tagacccgga ccagctcccc 1080  
 tcaaaaagaa gacactgtct catgggcctg tgctgtcacg agaggaacag ctgccccctc 1140  
 tgggcccgtt ggtgagaggt ttggtttgat acctctgcct cctcctgcc agcatggatt 1200  
 ctgggtggac acagccttgt ggaagggtcca gtaccaccaa gagctgcca tccactccca 1260  
 cccacactg tatcaaatgt atcacatttt ctcatgttga acacttttagc cttaattgaa 1320  
 aatgagcaac aaagtggac aattgctagt tgtatataaa atttaattc accgaatgta 1380  
 cagttttcaa atttcacgtg tatattaagg aactgatgca tctgagcatt ctgaaagaaa 1440  
 gaaaaagaag ctacttttagc tgccacccca ttctagaaaa gtctcttatt ttcaagctgt 1500  
 tctaaatagc ttcgtctcag tttcccaaaa aggggtacct agggccctcc tctgtgtgac 1560  
 ccagctgcat cagccagctt ctagggtggt ccattgtttt ctgccacctg acaacatttt 1620  
 tcttcaatta ctgtacaact actgtataaa ataaaacaac tactgtataa aataaactct 1680  
 ctcttttccc tggaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
 aaaaaaaaaa aaaaaaaaaa a 1761

&lt;210&gt; 71

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

Met Ala Thr Trp Asp Glu Lys Ala Val Thr Arg Arg Ala Lys Val Ala  
 1 5 10 15

Pro Ala Glu Arg Met Ser Lys Phe Leu Arg His Phe Thr Val Val Gly  
 20 25 30

Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp Glu Asn Glu  
 35 40 45

Glu Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr Pro Val Ser Gly  
 50 55 60

Glu Glu Gly Arg Ala Ala Ala Pro Asp Val Ala Pro Ala Pro Gly Pro  
 65 70 75 80

Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly Met Leu Arg Lys Leu Phe  
 85 90 95

Ser Ser His Arg Phe Gln Val Ile Ile Ile Cys Leu Val Val Leu Asp  
 100 105 110

Ala Leu Leu Val Leu Ala Glu Leu Ile Leu Asp Leu Lys Ile Ile Gln  
 115 120 125

Pro Asp Lys Asn Asn Tyr Ala Ala Met Val Phe His Tyr Met Ser Ile  
 130 135 140

Thr Ile Leu Val Phe Phe Met Met Glu Ile Ile Phe Lys Leu Phe Val  
 145 150 155 160

Phe Arg Leu Glu Phe Phe His His Lys Phe Glu Ile Leu Asp Ala Val  
                     165                    170                    175  
 Val Val Val Val Ser Phe Ile Leu Asp Ile Val Leu Leu Phe Gln Glu  
                     180                    185                    190  
 His Gln Phe Glu Ala Leu Gly Leu Leu Ile Leu Leu Arg Leu Trp Arg  
                     195                    200                    205  
 Val Ala Arg Ile Ile Asn Gly Ile Ile Ile Ser Val Lys Thr Arg Ser  
                     210                    215                    220  
 Glu Arg Gln Leu Leu Arg Leu Lys Gln Met Asn Val Gln Leu Ala Ala  
                     225                    230                    235                    240  
 Lys Ile Gln His Leu Glu Phe Ser Cys Ser Glu Lys Glu Gln Glu Ile  
                     245                    250                    255  
 Glu Arg Leu Asn Lys Leu Leu Arg Gln His Gly Leu Leu Gly Glu Val  
                     260                    265                    270

Asn

<210> 72  
 <211> 928  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (367)

<220>  
 <221> unsure  
 <222> (448)

<220>  
 <221> unsure  
 <222> (467)

<220>  
 <221> unsure  
 <222> (508)

<220>  
 <221> unsure  
 <222> (539)

<400> 72  
 aatcgaggagt cctggaaagt taattccaat gtcattgacgt caaacttaaa atggctcgtct 60  
 gccaccatga agattgataa ccctcacata acatatactg ccagggtccc agtcgatgtc 120  
 catgaatata acctaacgca tctgcagcct tccacagatt atgaagtgtg tctcacagtg 180  
 tccaatattc atcagcagac tcaaaaagtca tgcgtaaatg tcacaaccaa aaatgccgcc 240  
 ttgcagtggtg acatctctga tcaagaaacc agtacagccc ttgctgcagt aatggggtmt 300  
 atgtttgccg tcattagcct tgcgtccatt gctgtggtac tttgccaaaa gatttaagag 360  
 aaaaaantac caccactcat taaaaaagta tatgcaaaaa acctcttcaa tcccactaaa 420  
 tgagctgtac ccaccactca ttaacctntg ggaaggtgac agcgagnaag acaaagatgg 480

ttttgcagac accaagccaa cccaggtna cacatccaga aggtattaca tgtggttaant 540  
 cagaggatat ttgtctctg gtagtaagga gcacaaagac gtttttgctt tattctgcaa 600  
 aagtgaacaa gttgaagact ttgtatttt tgactttgct agtttggtgc agagtggaga 660  
 ggacgggtgg atatttcaaa tttttttagt atagcgtatc gcaagggttt gacacggctg 720  
 ccagcgactc taggcttcca gtctgtgttt ggtttttatt cttatcatta ttatgattgt 780  
 tattatatta ttattttatt ttagttgttg tgctaaactc aataatgctg ttctaactac 840  
 agtgctcaat aaaatgatta atgacaggat ggggttcccc tgtgctttta ccagtagcat 900  
 gacccttctt gaagccatcc gtagaaag 928

<210> 73

<211> 52

<212> PRT

<213> Homo sapiens

<400> 73

Met Ile Val Ile Ile Leu Leu Phe Tyr Phe Ser Cys Cys Ala Lys Leu  
 1 5 10 15

Asn Asn Ala Val Leu Thr Thr Val Leu Asn Lys Met Ile Asn Asp Arg  
 20 25 30

Met Gly Phe Pro Cys Ala Phe Thr Ser Ser Met Thr Leu Pro Glu Ala  
 35 40 45

Ile Arg Arg Lys  
 50

<210> 74

<211> 49

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (9)

<400> 74

aaattaaana aaaaaaaaaa aaaaaaaaaa aaataaagaa aaaaaaaaaa 49

<210> 75

<211> 597

<212> DNA

<213> Homo sapiens

<400> 75

attctacaag ataacttccc agtacttttaaaaagtctca aagtcataaa caagaaagaa 60  
 ctgagggact attgcatatt ggagcgatct aaagaagtat tacaatttgt ggaattcttg 120  
 attaaatcct ggaccagcaa aaggacatta gtgggaaaat tgatgaaatt caaatgagat 180  
 cttatattga agttaattgt gtcagtgtag atttccctggg tttcataatt gcaagtgtat 240  
 atgtaagggt tgtaaatatt aggagcagct gggtaaaggt tatacaaaaa ctctatacta 300  
 tttttgcatt tttttctgta agtttaaaac attttccaac taaaaagttg aaaacacatg 360  
 tattagagac acatgcgtat gtgtctctaa taatctttaa tatattttaag atgatagaag 420  
 gaattcttga gatagtaaaa tgaagtcacc aaaaaacaaa caaagaaaca aaacgaaatc 480  
 accaaaatct atcaataaat ttcaggtaat acttttggca gattcattcc tttagatggg 540  
 agtctcactc ccagtcctggg caacgagcga aactccgtct aaaaaaaaaa aaaaaaa 597

<210> 76

<211> 89

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

Met Arg Ser Tyr Ile Glu Val Asn Cys Val Ser Val His Phe Leu Val  
 1 5 10 15

Phe Ile Ile Ala Ser Asp Tyr Val Arg Phe Val Asn Ile Arg Ser Ser  
 20 25 30

Trp Val Lys Val Ile Gln Lys Leu Tyr Thr Ile Phe Ala Phe Phe Ser  
 35 40 45

Val Ser Leu Lys His Phe Pro Thr Lys Lys Leu Lys Thr His Val Leu  
 50 55 60

Glu Thr His Ala Tyr Val Ser Leu Ile Ile Leu Asn Ile Phe Lys Met  
 65 70 75 80

Ile Glu Gly Ile Leu Glu Ile Val Lys  
 85

&lt;210&gt; 77

&lt;211&gt; 1804

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1794)

&lt;400&gt; 77

ggagttcatt aggccagtgg cactgatttt tcttcccat catagctatt tattctagta 60  
 agaggataat aaaagaaatt tcctatacaa gaactgaaat tttccatttg tatggatcta 120  
 gtcactttca gattttcaatt tgaggttaag tatataaagc acatcccaat tttatatgct 180  
 gccttgagaa aattacagga tgcacggcaa tttgtaggaa tttcaaatgg gatcatttaa 240  
 acatttgaaa aattatttta aaaaccatct agtttgcttt tggatttttag acattaaagc 300  
 ctatgttgtc ttgttaacag ggggtggaatg tataaccatc agattcagca tgtgatttca 360  
 cctttgaatc tgagtatttc ttcctatct tctttgagtc atttttgag cagactgtca 420  
 ccagtattga taactaagca ttaaaggga aagttgcatt gcaactatgc attgggttcc 480  
 tgggaagaact tttcttttgt tttagtgaat gaagaggctt gatgggatca cttactgtaa 540  
 ctctctctac ataaggaccc ctcttgcaag cagaacacaa aagaacatgc tcaaggagta 600  
 tcccattttc tggataaatt gaagaagttt gctagtaaat tctttatact agcgtcttcc 660  
 ttgtatccct ttgctggcaa gggaatataa ggcgtcaaga ccacagatca aaacacccca 720  
 catttgagtg gagtcttatt tttactccaa gagcagttat tcccttctag tctaaaattg 780  
 gcagtttttt ctttttttta ataaaatttt taaaatattc ccaaaccagt ggaacacaga 840  
 cactggctgc acttagtact gccaaaagcc aaggtcattt gcacatatc catcaacctg 900  
 tcgagaatta ggcctcactt tataacccaa ggcattggaag tgcattgcatt ctcttagctg 960  
 ggcaacaat tatactgtag ttgtgataca acacatgttg cttttatttg tactgcacat 1020  
 atccactgta cagccacttg ggagtatcgt ggtagcttg cagcaactgc tgtctgcatt 1080  
 tatactgttt attgcatatt cttttccctg gaagtgaag agaaatgttt tcttggttgc 1140  
 attgattaca ttttataaat ttgcttagct ggaaagtgtt ggaaaagagg cctgtttgtc 1200  
 aattgtacaa cagattgtga agctctagt tgaatatttt tacgtctgta ttagacattt 1260  
 tctttgcaaa tctattgttc gattgaaatg taaatgaaat taaagatggg gtacacccat 1320  
 catgtaaaaa gcaggcacca tctctaagat ggatttaaat ctcattttta aggcataatac 1380  
 tcagcttcta tttaaaacta taatttaaaa taattctgta caatgaaatg gggaatatat 1440  
 atgggaataa attctattcc atttatttca atttgattt ccaaatgtga atgtttccct 1500  
 ttgtgctata ggaataggat taaatggggg aagactagga tttataagc ctgtatatgg 1560  
 ggggagggca gagatggaac aatgaggggt gtgatgatag tgaatagcaa agagtgaatt 1620  
 ctgtgtgttt ttgctgtagc actgaagtga agagatatta gctttggctg ttcacaaaat 1680

agagcatcat gatttttcagt gtttgagaga aaattgatgg aaaaagtttg cagtacttga 1740  
 catgtatttg catgcacaaa ataaaattat ttgtccacct taaaaaaaaa aaanaaaaaa 1800  
 aaaa 1804

<210> 78  
 <211> 37  
 <212> PRT  
 <213> Homo sapiens

<400> 78  
 Met Lys Arg Leu Asp Gly Ile Thr Tyr Cys Asn Ser Phe Tyr Ile Arg  
 1 5 10 15  
 Thr Pro Ser Ala Ser Arg Thr Gln Lys Asn Met Leu Lys Glu Tyr Pro  
 20 25 30  
 Ile Phe Trp Ile Asn  
 35

<210> 79  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 79  
 agaataccaa gactgtgtgt acacgcagat gtcagtggca gagaatgaag atcaqcttca 60  
 tgcaaagggt tatgacaaaa caccagactt cattttacaa gtaccagttg ctgtagaagg 120  
 gcacataatt cactggattg aaagcaaagc ctcatttggg gatgaatgta gccaccacgc 180  
 ctacctgcat gaccagttct ggagctactg gaataggggc ccaatataac agacaaatgg 240  
 tgaaacagag ggatactcac taggaaacag atttggggcca ggcttagtca tctattggta 300  
 tggatttacc caggagctgg actgcaaccg ggaaaggggc atcctgctca aagcctgttt 360

<210> 80  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
 Met Asp Leu Ser Arg Ser Trp Thr Ala Thr Gly Lys Gly Ala Ser Cys  
 1 5 10 15  
 Ser Lys Pro Val  
 20

<210> 81  
 <211> 202  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (136)

<220>  
 <221> unsure  
 <222> (138)

<400> 81

```

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 120
aaaaaaaaa aaaaantnaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 180
aaaaaaaaa aaaaaaaaaa aa                                     202

```

<210> 82  
 <211> 1189  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (1155)

```

<400> 82
ggccttcctg gcctaatacag atttttagtgg caagacaggt gatgataggg agaaagaaaag 60
agtcctgcct gtcaaaaagt gctgtgctat ataratgaac cctcacaggt agcacctctc 120
agagagaata ratggtaaat gtttcttttc aggtctttta aagtgtcagg ctatcagtta 180
acctctccta gatctcagaa atgcctagaa agagaagtcc tggctacatc aatggaaatt 240
ctccacagat gcaaattttc tctacaaaag atggcttttg agagccacct cagtctgttg 300
tccctgtagc agccatttca aattatgtca aagagatata ttttggggta aaatattttg 360
attatcttca ttagtatatc tcaattttgt caatacaaac ctgagagtta tagtcagagg 420
ttgaattttc atttcaaaat gttttcctag ttttttttct cttttttgtt ttattgtaag 480
ttgacaattt ataattgtat aaaagtatga ggtacaaagt gatgttatag cttaagaata 540
cagtatggta tgattaaatc aagttattaa cctatccttc acgttaaatg cttaaatatt 600
ttgatgagaa catttgaaat ttactcttgg aaggtaaaaa aaaatctcag gaccccccaa 660
attaaaagcca tgaagctgaa ttgtgcaaca tctcttcca aatggaagct tgtcttccag 720
gtacagaaca aaaacaagac tcatttcttc acctgcctaa agatgtgcac ataattggct 780
cctcctttac tccctttttc tcttctaaca ttcattatat cttgtgtaaa atgtagattt 840
actggacact aactaaaatt tcacagggtt gtaccattt gccttactgc ctacctacct 900
gtyttcttac gtaccttytc cccactttta ggaatgcata catattaaac ctcccaaaaa 960
cytytttaga aaaatagcca caggtttatt tgtggctggg gtgttttccc agatgcacty 1020
taaagctggc ttaataaacc tcagtgttgg aaacttatgc ctcaatcact cattttgggt 1080
gtcactgtct taccaatttg aaatgtaaaa tattytacta ctaattatat ttaccacatt 1140
gtgcaacaga actcnaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa          1189

```

<210> 83  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

```

<400> 83
Met Arg Thr Phe Glu Ile Tyr Ser Trp Lys Val Lys Lys Asn Leu Arg
  1             5             10             15

Thr Pro Gln Ile Lys Ala Met Lys Leu Asn Cys Ala Thr Ser Ser Ser
      20             25             30

Lys Trp Lys Leu Val Phe Gln Val Gln Asn Lys Asn Lys Thr His Phe
      35             40             45

Phe Thr Cys Leu Lys Met Cys Thr
      50             55

```

<210> 84  
 <211> 525  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 84

cataacagcg tcagagagaa agaactgact gaaacgtttg agatgaagaa agttctcctc 60  
 ctgatcacag ccatcttggc agtggctggt ggtttcccag tctctcaaga ccaggaacga 120  
 gaaaaaagaa gtatcagtga cagcgatgaa ttagcttcag gggtttttgt gttcccttac 180  
 ccatatccat ttgcccact tccaccaatt ccatttccaa gatttccatg gtttagacgt 240  
 aattttccta ttccaatacc tgaatctgcc cctacaactc cccttcctag cgaaaagtaa 300  
 acaagaagga aaagtcacga taaacctggt cacctgaaat tgaaattgag ccacttcctt 360  
 gaagaatcaa aattcctggt aataaaaagaa aaacaaatgt aattgaaata gcacacagca 420  
 ttctctagtc aatatcttta gtgatyttyt ttaataaaca tgraagcaaa graaaaaaaa 480  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 525

&lt;210&gt; 85

&lt;211&gt; 85

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 85

Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val  
 1 5 10 15

Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser  
 20 25 30

Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr  
 35 40 45

Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe  
 50 55 60

Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro  
 65 70 75 80

Leu Pro Ser Glu Lys  
 85

&lt;210&gt; 86

&lt;211&gt; 349

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (9)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (159)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (188)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (230)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (232)

<220>  
 <221> unsure  
 <222> (270)

<400> 86  
 acttcgcanc ccattcccggc tggacgcgac cggggagtgac agcagcccgt tccccctctc 60  
 ggtgcccgcct ctgcccagcg tttgcttggc tgggctacca cctgcgctcg gacggcgctc 120  
 ggagggtcct cgccccggc ctgcctacct gaaaaccana actgatggct ctatttgag 180  
 tctttcanac aacattcttc ttaacattgc tgccttgag gacttaccan antgaagtct 240  
 tggctgaacg tttaccattg actcctgttn tcacttaaag tttccaccaa ttctacgcgt 300  
 cagagtttgc acttacaatg gactgtccac aaccttcctt atcatcagg 349

<210> 87  
 <211> 563  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (63)

<220>  
 <221> unsure  
 <222> (83)

<220>  
 <221> unsure  
 <222> (116)

<220>  
 <221> unsure  
 <222> (177)

<220>  
 <221> unsure  
 <222> (183)

<220>  
 <221> unsure  
 <222> (228)

<220>  
 <221> unsure  
 <222> (240)

<400> 87  
 tccattccag caccagccaa cagcacaaaa ttaatccttg acaggtgttc ctaccaaatt 60  
 tngtcatag ccaacaacag tnggggtgct tctcctgctt ctgtaatagt catttntgca 120  
 gaccccgaaa acaaaagaggt tgaggaagaa agaattgcag gcacagaggg tggattnttt 180  
 ttnttttgga aaccccaacc tggagatgtt ataggttatg ttgtggantg gtgtgaccan 240  
 acccaggatg tgcctcggtg atttccagtg gaagaatgta ggtcccaata ccacaagcac 300  
 agtcattagc acagatgctt ttaggccagg agttcgatat gacttcagaa tttatgggtt 360  
 atctacaaaa aggattgctt gtttattaga gaaaaaaaac aggatactct caggaacttg 420  
 ctcttcaga caaccctcac gtgctggtgg atacattgac atcccaactcc ttcactctga 480  
 gttggaaaaga ttactctact gaatctcaac ctgggtttat acaagggtac catgtctatc 540  
 tgaaatccaa ggcgaggcag tgc 563

<210> 88  
 <211> 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 88

Arg Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala Pro Ser Asp Asn Pro  
 1 5 10 15

His Val Leu Val Asp Thr Leu Thr Ser His Ser Phe Thr Leu Ser Trp  
 20 25 30

Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly Tyr His  
 35 40 45

Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys  
 50 55

&lt;210&gt; 89

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (102)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (105)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (153)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (186)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (191)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (252)..(253)

&lt;400&gt; 89

gaaaaggcag ttcttttcaga tggtttcagaa tgttgcaaatt acaaaattga caaccgggaa 60  
 gaaaaggcat tgattgtgga caacctaaag ccagaatcct tntangagtt tttcatcact 120  
 ccattcacta gtgctgggta aggccccagt gcnacgttca cgaagggtcac gactccggat 180  
 gaacantcct ngatgetgat tcatatccta ctgcccattgg ttttctgcgt cttgctcact 240  
 atgggtcatgt gnnacttgaa aagtcagtgg atcaaggaga cctgttatcc tgacatccct 300  
 gacccttaca agagcagcat cctgtcatta ataaaattca aggtaaaaaa aaaaaaaaaa 360  
 a 361

&lt;210&gt; 90

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
 <221> unsure  
 <222> (37)

<220>  
 <221> unsure  
 <222> (54)

<220>  
 <221> unsure  
 <222> (376)

<220>  
 <221> unsure  
 <222> (433)

<400> 90  
 attgaattct agacctgcgg ccgctgctcc ctcagangcc cctgatgtct gganaattgt 60  
 gagcttgagg ccaggaaatc atactgtgac cttattctgg aagccattat caaaactgca 120  
 tgccaatgga aagatcctgt tctataatgt agttgtagaa aacctagaca aaccatccag 180  
 ttcagagctc cattccattc cagcaccagc caacagcaca aaactaatcc ttgacaggtg 240  
 ttccetaccaa atctgcgtca tagccaacaa cagtgtgggt gcttctcctg cttctgtaat 300  
 agtcatytct gcagaccccg aaaacaaaga gggttgaggaa gaaagaattg caggcacaga 360  
 ggggtggattt ttttntttt ggaaacccca acctggagat gttatagggt atgttgtgga 420  
 ctgggtgtgac canaccaggt atgtgcctcg gtgatttcca gtggaagaat gtaggtccca 480  
 ataccacaag cacagtcatt agcacagatg cttttaggcc aggagtccga tatgacttca 540  
 gaatttatgg gttatctaca aaaaggattg cttgtttatt agagaaaaaa aacaggatac 600  
 tctcaggaaac ttgtccttc agacaaccct cacgtgctgg tggatacatt gacatccac 660  
 tccctcactc tgagttggaa agattactct actgaatctc aacctgggtt tatacaaggg 720  
 taccatgtct atctgaaatc caaggcgagg cagtgc 756

<210> 91  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<400> 91  
 Arg Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala Pro Ser Asp Asn Pro  
 1 5 10 15  
 His Val Leu Val Asp Thr Leu Thr Ser His Ser Phe Thr Leu Ser Trp  
 20 25 30  
 Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly Tyr His  
 35 40 45  
 Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys  
 50 55

<210> 92  
 <211> 79  
 <212> DNA  
 <213> Homo sapiens

<400> 92  
 tcattaataa aattcaaggt aaatgttaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60  
 aaaaaaaaaa aaaaaaaaaa 79

<210> 93

<211> 1939  
 <212> DNA  
 <213> Homo sapiens

<400> 93  
 attggttttc aaatattaaa ccagcatttt attttaaaat aaaccccact tagttatgat 60  
 attttatctt ttttatataa tgtgggattt gatttgccga tattttatta aagatttttg 120  
 catcatgttc tttttctgaa attttatttt gttctaattg cataaaataa gttggaaatt 180  
 atcctctcta tctctacttt gtgaaagaat ttatattaca ttggtattat ctcttccttg 240  
 aatgtttgat agactatact agtgaaagca tctgggccta gggttttctc tgtggaagat 300  
 tttcagttac aaattcaatt ttactgagtc aggtttgata agttacattt ctcaaggaat 360  
 ttatctattt aatcattgaa tgtattgaac attcatttgt ttataaattt gttttgttat 420  
 tgaaaatgtc tgttaagattt atagtgatgt tcccttttct attcctgaca ttgttaattt 480  
 gtgttctctc tccctccatc cctctctcac tctctcttgt cagctgggtc gtgggattat 540  
 cacccttatt aatcttttca gagaaccact ttttatttct ttgatttctt ttattgtttg 600  
 ttaacttttt agtttattga tccctctctt tagctttatt acttcccttc tctacttag 660  
 taagagttaa attttccctc atttttttag cttcttaagg taggaaattt gattatattt 720  
 taaacttaaa aaaacttaaa gctataaaat tccctttaag cactgtttta gctgaattct 780  
 acatatattg attgggtatg ttttcatcat tcaactaaaa acatagtttc taattttttc 840  
 ttgcaatttc ttctttaacc cataggttat ttggcagttt gctgctgaat tccaaagtgc 900  
 ttgggaggtt ttatagctat cttgttaaaa attgatttct aatttaattt tgtcagagaa 960  
 catactttgt atgacttaaa tcttttaaaa tacgttcaga ctgatttagg gtccagcata 1020  
 tggtagctct tagtgaatgt aatatatgcc attggaaatg atgcacattc tgcaattgtt 1080  
 ggttgtaatg tgcataaaat gtcaaccagg ttaacttggg tgatagtatt gttgaattcc 1140  
 tgtgttccaa atgatatttt ttgtctgttt attctatcaa ttaatgagaa aggtttatta 1200  
 aaatctccaa ccattgttgt gcattttatt ctatttcttt agttctgttg atttttgttt 1260  
 tatatatatt gaagctctga gtacatctcc ctgatgagtt gacctttta tcattatgaa 1320  
 atgtcattct tctctctgaa tgcctatctt aaaatctact ttgtttgata tgaatgtagc 1380  
 cacttaagct tcttatgca tactgtttgc aaagtgtgtg tgtgtgtgtg tgtgtgtgtg 1440  
 tgtatctatc tcaatccttt agtttccgcc tatctctgtc tttttattta aagtgtgttt 1500  
 ttgcaggtag tgcataactt ggtatcttgt tttatattca gtctgacaa ttatgtctct 1560  
 tgattattgt gtttagttta ttgcatagt gtgtagtcca ttgacatttg gcataatatt 1620  
 gataatttgt gttggagcgt attgtcttca tttctgattg tcccatctgg tttgtgtgt 1680  
 gttttgttgt tctctgttc cacacttttt gtcttctttt gggttaatca aatattcttt 1740  
 ggctttgcat cttatgtctt ctgttggtt tttatctata ccttgtcgtt tttttcttta 1800  
 gtgtttctc taggggttac actatacatt attaatcaat catagtccat ttagaattaa 1860  
 tattgtacac ttacataaa atgtaaaaca ttgtcacag tataaagtct attccttcca 1920  
 aaaaaaaaaa aaaaaaaaaa 1939

<210> 94  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 94  
 Met Ser Val Arg Phe Ile Val Met Phe Pro Phe Leu Phe Leu Thr Leu  
 1 5 10 15  
 Leu Ile Cys Val Leu Ser Pro Ser Ile Pro Leu Ser Leu Ser Leu Val  
 20 25 30  
 Ser Trp Ser Val Gly Leu Ser Pro Leu Leu Ile Phe Ser Glu Asn His  
 35 40 45  
 Phe Leu Phe Leu  
 50

<210> 95  
 <211> 1252

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

```

gtagaaatcc caaaaagatt tggacagagg cagagcctat gtcactacac cttaaaggat 60
aacaagggtt' atatcaagac tcatggtgaa catgtagggt ttagaatttt catggatgcc 120
atactacttt ctttgactag aaaggtgaag atgccagatg tggagctctt tgttaatttg 180
ggagactggc ctttggaana aaagaaatcc aattcaaaca tccatccgat cttttcctgg 240
tgtggctcca cagattccaa ggatatcgtg atgcctacgt acgatttgac tgattctggt 300
ctggaaacca tgggcccggg aagtctggat atgatgtccg tgcaagctaa cacgggtcct 360
ccctgggaaa gcaaaaattc cactgccgtc tggagagggc gagacagccg caaagagaga 420
ctcgagctgg ttaaactcag tagaaaacac ccagaactca tagacgctgt tttaccaaac 480
tttttcttct ttaaacacga tgaaaacctg tatggtccca ttgtgaaaca tatttcattt 540
tttgatttct tcaagcataa gtatcaaata aatatcgtat gactgttagc agcttatcgc 600
ctggcatatt tgctagtggg tgacagtgtt gtgctgaagc aggattccat ctactatgaa 660
cattttttaca atgagctgca gccctggaaa cactacattc cagttaagag caacctgagc 720
gatctgctag aaaaacttaa atgggcgaaa gatcacgatg aagaggccaa aaagatagca 780
aaagcaggac aagaatttgc aagaaataat ctcattggcg atgacatatt ctgttattat 840
ttcaaaacttt tccaggaata tgccaattta caagtgaagt agccccaaat ccgagagggc 900
atgaaaaggg tagaaccaca gactgaggac gacctcttcc cttgtacttg ccataggaaa 960
aagaccaaag atgaactctg atatgcaaaa taacttctat tagaataatg gtgctctgaa 1020
gactcttctt aactaaaaag aagaattttt ttaagtatta attccatgga caatataaaa 1080
tctgtgtgat tgtttgcagt atgaagacac atttctactt atgcagtatt ctcagtactg 1140
tactttaaag tacattttta gaattttata ataaaaccac ctttatttta aaggaaaaaa 1200
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1252

```

&lt;210&gt; 96

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

```

Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys Val Lys Met Pro Asp
 1             5             10            15

Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro Leu Glu Lys Lys Lys
      20             25             30

Ser Asn Ser Asn Ile His Pro Ile Phe Ser Trp Cys Gly Ser Thr Asp
      35             40             45

Ser Lys Asp Ile Val Met Pro Thr Tyr Asp Leu Thr Asp Ser Val Leu
      50             55             60

Glu Thr Met Gly Arg Val Ser Leu Asp Met Met Ser Val Gln Ala Asn
      65             70             75             80

Thr Gly Pro Pro Trp Glu Ser Lys Asn Ser Thr Ala Val Trp Arg Gly
      85             90             95

Arg Asp Ser Arg Lys Glu Arg Leu Glu Leu Val Lys Leu Ser Arg Lys
      100            105            110

His Pro Glu Leu Ile Asp Ala Ala Phe Thr Asn Phe Phe Phe Phe Lys
      115            120            125

His Asp Glu Asn Leu Tyr Gly Pro Ile Val Lys His Ile Ser Phe Phe
      130            135            140

Asp Phe Phe Lys His Lys Tyr Gln Ile Asn Ile Asp Gly Thr Val Ala

```

Leu

```
<400> 97
ctagggttctg ggaagatggc gaaggtctca gagctttacg atgtcacttg ggaagaaatg 60
agagataaaa tgagaaaatg gagagaagaa aactcaagaa atagtgagca aattgtggaa 120
gttgagagaag aattaattaa tgaatatgct tctaagctgg gagatgatat ttggatcata 180
tatgaacagg tgatgattgc agcactagac tatggtcggg atgacttggc attgttttgt 240
cttcaagagc tgagaagaca gttccctggc agtcacagag tcaagcgatt aacaggcatg 300
agatttgagtg ccatggaaag atatgatgat gctatacagc tatatgatag gattttacaa 360
gaagatccaa ctaacactgc tgcaagaaa gctaagattg ccattcgaaa agcccagggg 420
aaaaatgtgg aggccattcg ggagctgaat gagtatctgg aacaatttgt tggagaccaa 480
gaagcctggc at                                     492
```

```
<210> 98
<211> 159
<212> PRT
<213> Homo sapiens
```

```

<400> 98
Met Ala Lys Val Ser Glu Leu Tyr Asp Val Thr Trp Glu Glu Met Arg
  1             5             10             15
Asp Lys Met Arg Lys Trp Arg Glu Glu Asn Ser Arg Asn Ser Glu Gln
      20             25             30
Ile Val Glu Val Gly Glu Glu Leu Ile Asn Glu Tyr Ala Ser Lys Leu
      35             40             45

```

Gly Asp Asp Ile Trp Ile Ile Tyr Glu Gln Val Met Ile Ala Ala Leu  
 50 55 60  
 Asp Tyr Gly Arg Asp Asp Leu Ala Leu Phe Cys Leu Gln Glu Leu Arg  
 65 70 75 80  
 Arg Gln Phe Pro Gly Ser His Arg Val Lys Arg Leu Thr Gly Met Arg  
 85 90 95  
 Phe Glu Ala Met Glu Arg Tyr Asp Asp Ala Ile Gln Leu Tyr Asp Arg  
 100 105 110  
 Ile Leu Gln Glu Asp Pro Thr Asn Thr Ala Ala Arg Lys Arg Lys Ile  
 115 120 125  
 Ala Ile Arg Lys Ala Gln Gly Lys Asn Val Glu Ala Ile Arg Glu Leu  
 130 135 140  
 Asn Glu Tyr Leu Glu Gln Phe Val Gly Asp Gln Glu Ala Trp His  
 145 150 155

<210> 99  
 <211> 85  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (20)

<220>  
 <221> unsure  
 <222> (27)

<400> 99  
 ccttggttaaa taaaccatgn tgatttntta aacttgccaa aaaaaaaaaa aaaaaaaaaa 60  
 aaaaaaaaaa aaaaaaaaaa aaaaaa 85

<210> 100  
 <211> 313  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (68)

<220>  
 <221> unsure  
 <222> (108)

<220>  
 <221> unsure  
 <222> (137)

<220>  
 <221> unsure  
 <222> (288)



<400> 100  
 ccttggatta tctgaactaa aaattggaca gattgatcag ctggtaaaaa atctacttcc 60  
 tggatttngt aaaggcaaaa acatttcttc ccattggcat acatcccntg tctctgcaca 120  
 atccttcttt gaaaatnaat atggtaacct aaatatattt agtacattac gttcctcttg 180  
 cttgtatcga catcattcaa aagctcttca aagcatttgt tcaaactctc agtactggcc 240  
 agttttcata cagtctcggg gttttaaaac tttgaaatca aggacacnac gtctccagtc 300  
 tacctccgag aga 313

<210> 101  
 <211> 964  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (395)

<400> 101  
 gcttttccgg agcagagttg gagaatcttg tgaaccaggc tgcattaaaa gcagctgttg 60  
 atggaaaaga aatggttacc atgaaggagc tggagttttc caaagacaaa attctaattg 120  
 ggcttgaaag aagaagtgtg gaaattgata aaaaaacaa aaccatcaca gcatacatg 180  
 aatctgggtca tgccattatt gcataattaca caaaagatgc aatgcctatc aacaaagcta 240  
 caatcatgcc acggggggcca acacttggac atgtgtccct gttacctgag aatgacagat 300  
 ggaatgaaac tagagcccg ctgcttgac aaatggatgt tagtatggga ggaagagtgg 360  
 cagaggagct tatatttggg accgaccata ttacnacagg tgcttccagt gattttgata 420  
 atgccactaa aatagcaaa cggatrgyta ccaaatttgg aatgagtga aagcttggag 480  
 ttatgacct cagtgtatca ggggaaacta agtccagaaa cccaatctgc catcgaacaa 540  
 gaaataagaa tcccttctaag ggactcatat gaacgagcaa aacatatctt gaaaactcat 600  
 gcaaaggagc ataagaatct cgcagaagct ttattgacct atgagacttt ggatgccaaa 660  
 gagattcaaa ttgttctkga ggggaaaaag ttggaagtga gatgataact ctctkgatat 720  
 ggatgcttgc tggttttatt gcaagaatat aagtagcatt gcagtagtct acttttacia 780  
 cgttttcccc tcattcttga tgtggtgtaa ttgaagggtg tgaaatgctt tgtcaatcat 840  
 ttgtcacatt tatccagttt gggttattct cattaggaca cctattgcaa attagcatcc 900  
 catggcaaat atattttgaa aaaataaaga actatcagga ttgaaaaaaa aaaaaaaaaa 960  
 aaaa 964

<210> 102  
 <211> 166  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (125)..(126)

<400> 102  
 Met Val Thr Met Lys Glu Leu Glu Phe Ser Lys Asp Lys Ile Leu Met  
 1 5 10 15  
 Gly Pro Glu Arg Arg Ser Val Glu Ile Asp Asn Lys Asn Lys Thr Ile  
 20 25 30  
 Thr Ala Tyr His Glu Ser Gly His Ala Ile Ile Ala Tyr Tyr Thr Lys  
 35 40 45  
 Asp Ala Met Pro Ile Asn Lys Ala Thr Ile Met Pro Arg Gly Pro Thr  
 50 55 60  
 Leu Gly His Val Ser Leu Leu Pro Glu Asn Asp Arg Trp Asn Glu Thr

```
<210> 103
<211> 1362
<212> DNA
<213> Homo sapiens
```

```
<210> 104.  
<211> 86  
<212> PRT  
<213> Homo sapiens
```

64

Ile Glu Gln Ile Ile Met Phe Cys Phe Val Leu Phe Leu Phe Leu Tyr  
 20 25 30  
 Phe Arg Asn Ser Thr Ala Thr Tyr Lys Ser Ser Leu Glu Leu Ser Gly  
 35 40 45  
 Tyr Leu Lys Ser Glu Ala Ser Thr Phe Leu Arg Thr Lys His Arg Asn  
 50 55 60  
 Asp Glu Met Ser Tyr Lys Tyr Pro Phe Ile Leu Phe His Asn Thr Tyr  
 65 70 75 80  
 Ile Asp Leu Leu Tyr Val  
 85

<210> 105  
 <211> 479  
 <212> DNA  
 <213> Homo sapiens

<400> 105  
 ctggcttctt cggagctgtg taktcttaat ttgctttgct gctggctggc tgacagctga 60  
 tgggggactc ctcaggacgg actcccttcc agatgcaccc atctccatcc ttctcaactc 120  
 cccaaccttt gtctcccca ctcttegtc gcgcggcggc ctgagaccac caggaccagt 180  
 ttcaggggtt tccttctcca gcgagacttg gcagaacagg ctttaaaagc aaaggaggca 240  
 gcggaagact gtgaattcct ttggacaatt gatgatattt atcattgtgc ccagtttcta 300  
 caaataaaaag atgggtggat tattttctcg atggaggaca aaaccttcaa ctgtagaagt 360  
 tctagaaaagt atagataagg aaattcaagc attggaagaa tttagggaag aaaaaaaaaa 420  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 479

<210> 106  
 <211> 33  
 <212> PRT  
 <213> Homo sapiens

<400> 106  
 Met Gly Gly Leu Phe Ser Arg Trp Arg Thr Lys Pro Ser Thr Val Glu  
 1 5 10 15  
 Val Leu Glu Ser Ile Asp Lys Glu Ile Gln Ala Leu Glu Glu Phe Arg  
 20 25 30

Glu

<210> 107  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (70)

<220>  
 <221> unsure  
 <222> (156)

<220>  
<221> unsure  
<222> (184)

<220>  
<221> unsure  
<222> (207)

<220>  
<221> unsure  
<222> (308)

<400> 107  
ctgacttact aatactaaaag aagtgggggg agctcgagag ccagacggcc agacaggcag 60  
accctccan aggcccgcca ggtgggcatg gtccccatt ttctttaagg cagcacctgg 120  
agtggagaga ggccactccc tctccagccc ccgatntgga cccgggggag gggaggctga 180  
tgcntttggc cccggcctgg ccaaaanagc ccatccccag ggcagtttca ggtgccggct 240  
gggccctgaa tgtcaaggat aatatatagc ccgctcctgg gtccctggagc tgtggccctt 300  
tgtactcttg ttgtgtccat tgtgtgtgtg cgt 333

<210> 108  
<211> 611  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (62)

<220>  
<221> unsure  
<222> (185)

<220>  
<221> unsure  
<222> (192)

<220>  
<221> unsure  
<222> (249)

<220>  
<221> unsure  
<222> (290)

<400> 108  
gtccattgtg tgtgtgcgtg gggacagagg cctggaaatg cggaggacta tacagagaag 60  
gnagggtttg tgaaggccag gcagggttgg aggccggggg tgtgagagga gaggcccata 120  
gggctgagtg gggtcgggtg aggcagaggt cagaaacaga agagctgcag ttgctggagc 180  
tgggntgaga antgggctgc ctccctgceat ccccccgtct cctcccttc tccccttgg 240  
gccccctnt gctcagaatc tgaagtagtt ccctcctcag caatttcatt tcttgaacac 300  
tgactcacac ctttttaggca cctactgtgt gcatagcatt ccaccaggac tcatctccct 360  
tccttctcag ggggtcccga gcccgcacta gctttgcect aactccttca tcaaaagacc 420  
ccccgccagc ttcccacacc tcatacgcag ccacatctgc cctattctcc atgctttcca 480  
gcttgccctg ccttcctcat ctctccctgc ctgtgcagac ctccaccctt ctttcctcca 540  
ccctccate cccaatgct tgtagacctt ccattcattc cgtctcatcg tgcgtgggtc 600  
ctgatcgtcc a 611

<210> 109  
<211> 47

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

Met Leu Ser Ser Leu Pro Ala Leu Pro His Leu Ser Leu Pro Val Gln  
 1 5 10 15

Thr Ser Thr Leu Leu Ser Ser Thr Pro Pro Ser Pro Asn Ala Cys Arg  
 20 25 30

Pro Ser Ile His Ser Val Ser Ser Cys Val Val Ser Asp Arg Pro  
 35 40 45

&lt;210&gt; 110

&lt;211&gt; 274

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

atccagggcg tggggagacc attggcattt ggggaaccatt ttccttcgaa cggcttcccc 60  
 ttgagctgag cattctgctt gctgcagtag acgggtcgcc ttttgcccat accgaaattt 120  
 tctgaaatta aatcgcacac cccaccatt tctctcccc tgggatctgg aggaacatca 180  
 tacatagtag gtgaatcgtt ttgtagagtg aagaatgcta atgtaaagca aatagtcacc 240  
 cacgttccct tgtaaattcca aaaaaaaaaa aaaa 274

&lt;210&gt; 111

&lt;211&gt; 1646

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 111

catcgggtgg actagctggg atctccgcat tggatttggg gctgattacc actgcttgcc 60  
 tattattatt gttgtgttta ctactattat ttttttttac ccaagggaga aagacaaaaa 120  
 aacgggtggga tttatttaac atgatcttgg caaacgtctt ctgcctcttc tcttttctag 180  
 acgagaccct ccgctctttg gccagccctt cctccctgca gggccccgag ctccacggct 240  
 ggcgcccccc agtggactgt gtccgggcca atgagctgtg tgccgcccga tccaactgca 300  
 gctctcgcta ccgcactctg cggcagtgcg tggcaggccg cgaccgcaac accatgctgg 360  
 ccaacaagga gtgccaggcg gccttggagg tcttgcaagg gagcccgctg tacgactgcc 420  
 gctgcaagcg gggcatgaag aaggagctgc agtgtctgca gatctactgg agcatccacc 480  
 tggggctgac cgaggggtgag gagttctacg aagcctcccc ctatgagccg gtgacctccc 540  
 gcctctcgga catcttcagg cttgcttcaa tcttctcagg gacaggggca gaccgggtgg 600  
 tcagcgccaa gagcaaccat tgccctggatg ctgccaaggc ctgcaacctg aatgacaact 660  
 gcaagaagct gcgctcctcc tacatctcca tctgcaaccg cgagatctcg cccaccgagc 720  
 gctgcaaccg ccgcaagtgc cacaaggccc tgcgccagtt ctctgaccgg gtgccagcg 780  
 agtacacctc ccgcatgctc ttctgctcct gccaaagcca ggcgtgcgct gagcgccgcc 840  
 ggcaaaccat cctgccccagc tgctcctatg aggacaagga gaagcccaac tgcctggacc 900  
 tgcgtggcgt gtgccggact gaccacctgt gtcgggtccc gctggccgac ttccatgcca 960  
 attgtcgagc ctccctaccag acggtcacca gctgccctgc ggacaattac caggcggtgc 1020  
 tgggctctta tgctggcatg attgggtttg acatgacacc taactatgtg gactccagcc 1080  
 ccactggcat cgtgggtgtc ccctgggtgca gctgtcgtgg cagcgggaac atggaggagg 1140  
 agtgtgagaa gtccctcagg gacttcaccg agaaccctat cctccggaac gccatccagg 1200  
 ccttttgcaa cggcacggac gtgaacgtgt ccccaaaagg cccctcgttc caggccaccc 1260  
 agggccctcg ggtggagaag acgccttctt tgccagatga cctcagtgc agtaccagct 1320  
 tggggaccag tgtcatcacc acctgcacct ctgtccagga gcaggggctg aaggccaaca 1380  
 actccaaaga gttaagcatg tgcttcacag agctcacgac aaatatcacc ccaggaggta 1440  
 acaaggtgat caaacctaac tcaggcccca gcagagccag accgtcggct gccttgaccg 1500  
 tgctgtctgt cctgatgctg aaacaggcct tgtaggctgt gggaaaccgag tcagaagatt 1560  
 tttgaaagct acgcagacaa gaacagccgc ctgacgaaat ggaaacacac acagacacac 1620  
 acacaccttg caaaaaaaaaa aaaaaa 1646

<210> 112  
 <211> 464  
 <212> PRT  
 <213> Homo sapiens

<400> 112

```

Met Ile Leu Ala Asn Val Phe Cys Leu Phe Phe Phe Leu Asp Glu Thr
  1             5             10             15

Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Pro Glu Leu His
      20             25             30

Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
      35             40             45

Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
      50             55             60

Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
      65             70             75             80

Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
      85             90             95

Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
      100            105            110

His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr
      115            120            125

Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
      130            135            140

Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His
      145            150            155            160

Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
      165            170            175

Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
      180            185            190

Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe
      195            200            205

Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys
      210            215            220

Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser
      225            230            235            240

Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly
      245            250            255

Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His
      260            265            270

Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp
      275            280            285

```

Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp  
 290 295 300  
 Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Ile Val Val Ser  
 305 310 315 320  
 Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu  
 325 330 335  
 Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile  
 340 345 350  
 Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Val Ser Pro Lys Gly Pro  
 355 360 365  
 Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu  
 370 375 380  
 Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr  
 385 390 395 400  
 Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys  
 405 410 415  
 Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly  
 420 425 430  
 Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro  
 435 440 445  
 Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Gln Ala Leu  
 450 455 460

<210> 113  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (133)

<220>  
 <221> unsure  
 <222> (151)

<220>  
 <221> unsure  
 <222> (196)

<220>  
 <221> unsure  
 <222> (228)

<400> 113  
 ctctcatttt tccttttcgaa gtgatatcca ctggaacgag atcaaatctg taagctggag 60  
 atacaacttc cactacataa gatccagaag gtatatcatg aaccacaaaa ctcccatctg 120  
 tcttaaggaa acngacgtgc tcttctcgt ntaccagcac tcgggcccgc gagatccagt 180

cctgaggctt caccnttgga acaactgcac gcccctcaat cttgaagnga tctcctatgc 240  
 cgacccact cctcccgat ccctcagcag cagcccgagg cacctccgag ttctggacat 300  
 ccccgatag cagcagcagc agcaggacgg gaaagaagcc ccacagagcg gccgc 355

<210> 114  
 <211> 587  
 <212> DNA  
 <213> Homo sapiens

<400> 114  
 ggctggacag acttttctaata gaacccaatg gttatgatga tggttcttcc tttattgata 60  
 ttgtgtcttc tgcctaaagt ggtcaacaca agtgatcctg acatgagacg ggaaatggag 120  
 cagtcaatga atatgctgaa ttccaacat gagttgcctg atgtttctga gttcatgaca 180  
 agactcttct cttcaaaatc atctggcaaa tctagcagcg gcagcagtaa aacaggcaaa 240  
 agtggggctg gcaaaaggag gtagtcagcg cgtccaragc tggcatttgc acaaacacgg 300  
 caacactggg tggcatccaa gtcttgga accgtgtgaa gcaactacta taaacttgag 360  
 tcatcccgac gttgatctct tacaactgtg tatgttaact ttttagcaca tgtttgtac 420  
 ttggtacacg agaaaaccca gctttcatct tttgtctgta tgaggccaat attgatgtca 480  
 ctgaattaat tacagtgtcc tatagaaaat gccattaata aattatatga actactatac 540  
 attatgtata ttaattaaaa catcttaatc cagaaaaaaa aaaaaaa 587

<210> 115  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<400> 115  
 Met Asn Pro Met Val Met Met Met Val Leu Pro Leu Leu Ile Phe Val  
 1 5 10 15  
 Leu Leu Pro Lys Val Val Asn Thr Ser Asp Pro Asp Met Arg Arg Glu  
 20 25 30  
 Met Glu Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro Asp  
 35 40 45  
 Val Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly Lys  
 50 55 60  
 Ser Ser Ser Gly Ser Ser Lys Thr Gly Lys Ser Gly Ala Gly Lys Arg  
 65 70 75 80

Arg

<210> 116  
 <211> 601  
 <212> DNA  
 <213> Homo sapiens

<400> 116  
 gatgtaccta ggcaccgcgc agcctgcggc ccccaacacc acctcccccg agctcaacct 60  
 gtcccacccg ctcctgggca ccgccctggc caatgggaca ggtgagctct cggagcacca 120  
 gcagtacgtg atcggcctgt tcctctcgtg cctctacacc atcttctctt tccccatcgg 180  
 ctttgtgggc aacatcttga tcctgggtgt gaacatcagc ttccgcgaga agatgaccat 240  
 ccccgacctg tacttcatca acctggcggg gccggacctc atcctgggtg ccgactccct 300  
 cattgaggtg ttcaacctgc acgagcggta ctacgacatc gccgtcctgt gcaccttcat 360  
 gtcgctcttc ctgcagggtca acatgtacag cagcgtcttc ttcttcacct ggatgagctt 420  
 cgaccgctac atcgccctgg ccagggccat gcgctgcagc ctgttccgca ccaagcacca 480



cgccccggctg agctgtggcc tcactctggat ggcacccgtg tcagccacgc tgggtgccctt 540  
 caccgcccgtg cacctgcagc acaccgacga ggcctgcttc tgtttcgcgg atgtccggga 600  
 g 601

<210> 117  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

<400> 117  
 Met Tyr Leu Gly Thr Ala Gln Pro Ala Ala Pro Asn Thr Thr Ser Pro  
 1 5 10 15  
 Glu Leu Asn Leu Ser His Pro Leu Leu Gly Thr Ala Leu Ala Asn Gly  
 20 25 30  
 Thr Gly Glu Leu Ser Glu His Gln Gln Tyr Val Ile Gly Leu Phe Leu  
 35 40 45  
 Ser Cys Leu Tyr Thr Ile Phe Leu Phe Pro Ile Gly Phe Val Gly Asn  
 50 55 60  
 Ile Leu Ile Leu Val Val Asn Ile Ser Phe Arg Glu Lys Met Thr Ile  
 65 70 75 80  
 Pro Asp Leu Tyr Phe Ile Asn Leu Ala Val Ala Asp Leu Ile Leu Val  
 85 90 95  
 Ala Asp Ser Leu Ile Glu Val Phe Asn Leu His Glu Arg Tyr Tyr Asp  
 100 105 110  
 Ile Ala Val Leu Cys Thr Phe Met Ser Leu Phe Leu Gln Val Asn Met  
 115 120 125  
 Tyr Ser Ser Val Phe Phe Leu Thr Trp Met Ser Phe Asp Arg Tyr Ile  
 130 135 140  
 Ala Leu Ala Arg Ala Met Arg Cys Ser Leu Phe Arg Thr Lys His His  
 145 150 155 160  
 Ala Arg Leu Ser Cys Gly Leu Ile Trp Met Ala Ser Val Ser Ala Thr  
 165 170 175  
 Leu Val Pro Phe Thr Ala Val His Leu Gln His Thr Asp Glu Ala Cys  
 180 185 190  
 Phe Cys Phe Ala Asp Val Arg Glu  
 195 200

<210> 118  
 <211> 419  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (80)

<220>

&lt;221&gt; unsure

&lt;222&gt; (178)

&lt;400&gt; 118

```

acgcctgagc gtcctccatc ttccaggatg gcagcaatgg cgctgtgcgg cctcaccagg 60
cccacgagga gcagcagcgn tcggcccgga gcagcaggaa ggcccttttg tggagcgccc 120
gccgtctgct cgggggtggt tcagtcactg cttgttgaca tcaacatggc aattgcantc 180
atgtggactg ggaccgtgcg agctgccgtg tgggttagtc gggtgccagg acaatgaaat 240
actccagcac gtgtggctga cgaatttgtt ttacagaaa taacagctgg ggacaactgc 300
ggtgatgatg taaaaacctt ccataaaaat gtaagaaaag ctgatgaggc tggtgacgtt 360
cagcctttgt caataaacct gtcatgtgcg gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 419

```

&lt;210&gt; 119

&lt;211&gt; 714

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens .

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (646)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (649)

&lt;400&gt; 119

```

agccattggg acaggaaatg ccaaacaaca ccagataag gttgctgaag ccataattga 60
tgccattgaa gactttgtcc agaaaggatc agcccagtct gtgaaaaaag ttaaagtgtt 120
tatctttctg cctcaagtac tggatgtgtt ttatgccaac atgaagaaaa gagaaggagc 180
tcagctttct tcccaacagy ctartswtsy ytwmyttky akcatttttg ggcttttcaa 240
agcaatctcc ccaaaaaaag aatcatttgg ttttggaata gaaaacagaa tcagcaactt 300
ttcgggtgtg tgggtgaaaat gtcacgtgtg tggaatacgc tatctcctgg ctacaagacc 360
tgattgaaaa agaacagtgt ccttacacca gtgaagatga gtgcatcaaa gactttgatg 420
aaaaggagta tcaggagttg aatgagctgc agaagaagt aaatattaac atttccttgg 480
accataagag acctttgatt aaggttttgg gaattagcag agatgtgatg caggctagag 540
atgaaattga ggcgatgac aagagagtgc gattggccaa agaacaggaa tcccgggcag 600
attgtatcag tgagtttata gaatggcagt ataatgacaa taacantnt cattgtttta 660
acaaaatgac caatctgaaa ttagaggatg caaggagaga aaaaaaaaaa aaaa 714

```

&lt;210&gt; 120

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (141)..(142)

&lt;400&gt; 120

```

Phe Leu Gly Phe Ser Lys Gln Ser Pro Gln Lys Lys Asn His Leu Val
  1                      5                      10                     15

Leu Glu Lys Lys Thr Glu Ser Ala Thr Phe Arg Val Cys Gly Glu Asn
                20                      25                     30

Val Thr Cys Val Glu Tyr Ala Ile Ser Trp Leu Gln Asp Leu Ile Glu
                35                      40                     45

Lys Glu Gln Cys Pro Tyr Thr Ser Glu Asp Glu Cys Ile Lys Asp Phe
                50                      55                     60

```

Asp Glu Lys Glu Tyr Gln Glu Leu Asn Glu Leu Gln Lys Lys Leu Asn  
65 70 75 80

Ile Asn Ile Ser Leu Asp His Lys Arg Pro Leu Ile Lys Val Leu Gly  
85 90 95

Ile Ser Arg Asp Val Met Gln Ala Arg Asp Glu Ile Glu Ala Met Ile  
100 105 110

Lys Arg Val Arg Leu Ala Lys Glu Gln Glu Ser Arg Ala Asp Cys Ile  
115 120 125

Ser Glu Phe Ile Glu Trp Gln Tyr Asn Asp Asn Asn Xaa Xaa His Cys  
130 135 140

Phe Asn Lys Met Thr Asn Leu Lys Leu Glu Asp Ala Arg Arg Glu  
145 150 155

<210> 121

<211> 2681

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2656)

<400> 121

cataacttcc aatcttcttg gcctggcact aaggacctac tacagactgg cactgaaata 60  
tcttccctac cttatcattc cttgtgcttc tccacaagcc cactcttccc cttcatcata 120  
catgtgccga ccttctctgt cttctttact ttgcagcacc aaatgcttcc tactttgtgg 180  
tctaggagga acacatgtca cttttgtaag ctgctcgaaa gcaggggcca caccttcate 240  
cttgttttcc acacaacacc aagcacttag tagacaccca ataaatcatt gctgaatgaa 300  
tgtattcagc ctggaattgc actaggattt cttggccaac acattgtatt ctttaactgat 360  
accagacttc caatcaaata aaatccttaa gcctttttca tagtctttaa ttaaactact 420  
tctcttccat tatttccctt tgccctactt tgaactgata ttcagaactt ttctgttaat 480  
gtttaatttt catccattat tcttgctgtg acagatcttt ttgatttttg actctcttat 540  
ctagtttttt tttttttttt ttggcttccc gttgtgttat ccacaggcac aatgggtata 600  
ttgactatcg ttcattgaag ttgttgatac aaatgttgaa caggagaaaa accagtagct 660  
tgccaacttg gcacctcatt ctctagcttg acagtaatct cttatctagt agtttttaga 720  
tatggttatt taatcaaata tcaactagct ctaattttgt tataattcat tcatgtatac 780  
agacaatgaa gaatcatctt tcttcattca acacatttat tgggaaccaa tcattgtcca 840  
aggcaatatg ctaggcattg tgtaatagaa agcgattaaag cttttacccc tgtcctcttt 900  
ggcctgcaaa gagcaggtaa gattcatgca cagacaaatg tagtaccagg taaatagtga 960  
ggccaaacac aagaggcagg tcaaagggct ttggattcag aggatggaga agctctttct 1020  
aggctggtga aatatttgca gaatgagtag gtcataagt ggaggtgagg tacaggctaa 1080  
gctgctgtaa gaaagagtc aaatgcaaa ggatttacca caatgcagtt aattttcttc 1140  
acaacggtcg aggtaggcag gtgggtccaag tccagttaat cagccctcct caacacaagg 1200  
cttccccttg taagctcagg atgaccgctc cagtctctcat catctcccag gcagaaaaac 1260  
gggagaaaaga gaactagacg taccaccagc tcatttttaag gacatagcca ggccagggtg 1320  
agtgaactac atctgtaatc caagcacttt gggagggtcg aggctggagg atagcttgaa 1380  
gccaggagtt tgagaccagc ttggataaga aagcaagacc ttgtctctac aaaaaattta 1440  
aaaattaacc atgtgtggtg gtgtgcacct atagtcccag ctactcagga ggctgagggtg 1500  
gaaggatcac ttgagcacag gagttggagg atacagttag ccatgatcac accacctcac 1560  
tccagccttg gcaacatagt gagaccccat ctttttaaaa aacaaaacaa aaaaacatca 1620  
ccaggaagtt gcttacatgt cttctattcc tataacatcg gcctgagctt agtcacatgg 1680  
ccacaccag cagaaagaac tctaggaat atggtcttat gctaggtaac cccaaaccca 1740  
gctaaaactg ttgcttttga agaaggtgta aacagacaat gtggaggaga attaccagtc 1800

```

tgccacaaag agaaagaatt ctatgtgagg aaaacgctct agaagagggg gctgattaat 1860
tagttatatc tcagccgaga ggatgttatg agaaacacag atttgggttt aatagaaaaa 1920
cttagaaccc ttcaagaagg aatgggcgga cttgagagtg tcctccgctt ctgaaaatga 1980
tcaagaaaaa tggtaagaat gtacacctca aggggtggatg gtaaagggtca gcctttaagc 2040
ctcaatggcg gtgtggttgt aggtgggggtg ggggtggagg ccccgaaagc aggcagacta 2100
ccacagtagc cccgatggaa gcagtggaga tgaactggaa ggagcggctg tgggagcgac 2160
aacgtgatga gaataaaccc ggcttggttc tgccctgtgc acacacaggt gagctgtgtg 2220
ctcccggtatg tgtcagctgg tatatgcgtc tgtcagaagg cagctgggga gcactgttag 2280
ctcagagact aagaggcaga cccaggaagc ccttctttgc attggtcagg gtttgcgtca 2340
ttttcccaag cccaggaaat ggaaccagc tcttcttctt tctgtgtaaa ataataagca 2400
tcacaatagg ctgtgctcat gagaacgcac tttgtttcca cagaaatgtt ttttctcact 2460
ctgtcctgat tttgatttct gttaaactca gtaaacacat taccaaattt taaaataagg 2520
tgacttgttt tcccactc acagttcacc aaaggtatct catctgtttg ttctgaaaat 2580
gcagctgctg tctagattta tgtgtgctct gacaagaaat gttttgtgta acaataaaaa 2640
tcatttcctt tgatgnaaaa aaaaaaaaaa aaaaaaaaaa a 2681

```

&lt;210&gt; 122

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 122

```

Met Glu Ala Val Arg Met Asn Trp Lys Glu Arg Leu Trp Glu Arg Gln
  1              5              10             15

Arg Asp Glu Asn Lys Pro Gly Leu Ala Leu Pro Cys Ala His Thr Gly
          20              25             30

Glu Leu Cys Ala Pro Gly Cys Val Ser Trp Tyr Met Arg Leu Ser Glu
          35              40             45

Gly Ser Trp Gly Ala Leu Leu Ala Gln Arg Leu Arg Gly Arg Pro Arg
          50              55             60

Lys Pro Phe Phe Ala Leu Val Arg Val Cys Cys Ile Phe Pro Ser Pro
          65              70             75             80

Gly Asn Gly Thr Gln Phe Phe Phe Phe Leu Cys Lys Ile Ile Ser Ile
          85              90             95

Thr Ile Gly Cys Ala His Glu Asn Ala Phe Cys Phe His Arg Asn Val
          100             105            110

Phe Ser His Ser Val Leu Ile Leu Ile Ser Val Lys Leu Ser Lys His
          115             120            125

Ile Thr Lys Phe
          130

```

&lt;210&gt; 123

&lt;211&gt; 1585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 123

```

ctaagctatt tgattctagg tctagaatgt tatctcttat tagaggatat gttaattttc 60
ctgcatttta ttcatattat aacttaacat ctctgattgc ctaccatgtg tcaggctctg 120
tactaaggat tgaggaccca aagatgaaca aaacatgggg cctaattcaa agatttcaca 180
atctggagag aaagtcagcc acatacaaaa aattataagg tagaatgtgc tataaaaaat 240

```

```

gatttaggta cagtgggaagt ttagaaaggc ttcactaaag atgtcgtatt tgaattgggt 300
ctgagcatga attagctctc aggtgagggg ggggggttaa gaaaactcta atgaaggaac 360
tctagtatgt gtgaaggcaa ggaggctgggt gtgttttaggt tgcagcaaac caagtacaac 420
caggcttgga cttgagtgc tggaaagaca ggaagatgcc atgctgagaa aaactgccc 480
tgccaagctg agaaatgttc agcagaaaca taagggtgagc tgcataatgtc atttataaatg 540
ttctaggagc cacattttta aaaaatcaaa attaacaagt caaaaaataa aaagcaatgg 600
ggggagatta atgcatatt actaagtga agaagccaat caaaaaaggc tacataacctg 660
tatgattcca actatatgac attctgaaaa aggccaaact atagagacag taaatgatca 720
gtgggttgcca ggagtttaggg agggaggagg gatgaacagg cagagcacag aagattttta 780
gagcagtaga actattttgt atgatattat aatattgtag atacatatca ttataaattt 840
gtccaaacct atagaatgta caccaagagt gaactcta atgtaactgtg gactttgggt 900
gataaatgat tgtcagtgtg gattgatcag ttgtaacaaa tgtaccattc tgggtgggaa 960
tgttgataat ggagtaggct atgcatgtgt ggggcagtgg gtatatggga aatatctata 1020
ccttctgggc agtttttgc tgaacctgat ctaaaaata gcctactaag aaacacaagt 1080
caaatataatt ttaataatac attttattta acccaattta tcagaaatac taatattttta 1140
acatgtaatt gatataaaag ttattaacta gatattttac tttttttgggt actgagtctt 1200
tgaaatctgg tctgtatttt acattttacag tacatctcaa ttcacattag ccacatttca 1260
gatactcagt acatacatga gtacctatgg ctagtggctg ctgtgttgga cagggcagg 1320
cttgaacct ggacttgcct gactcagaag cctcaattct cagccacagt gatattcctg 1380
tccctaagta ctataatgat aaacacaaga ggagaggagc ttccagatga tcattctaac 1440
ccatgacgtt agctgtgtct ctccacactg cccggtggct ccagtctgaa gcattctagg 1500
agtgctgtcc aacagaaata caatgagagc caatacgtga taagtgtcct atgggccaca 1560
ttgaaacagt aaaaaaaaaa aaaaa 1585

```

&lt;210&gt; 124

&lt;211&gt; 63

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

```

Met Leu Ser Leu Ile Arg Gly Tyr Val Asn Phe Pro Ala Phe Tyr Ser
  1             5             10             15

```

```

Phe Ile Asn Leu Thr Ser Leu Ile Ala Tyr His Val Ser Gly Ser Val
      20             25             30

```

```

Leu Arg Ile Glu Asp Pro Lys Met Asn Lys Thr Trp Gly Leu Ile Gln
      35             40             45

```

```

Arg Phe His Asn Leu Glu Arg Lys Ser Ala Thr Tyr Lys Lys Leu
      50             55             60

```

&lt;210&gt; 125

&lt;211&gt; 625

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 125

```

gatccacca gttctgcctg gtttccctcca tccccagagg cactaaaagc agtattttta 60
gggtgggtgtc ttactccctg gaagcctgaa atgggtggaa tagcggttaag gcttgagtaa 120
aactagggga cagaggttct tatttgcga ttttatttta taatttgacc acagcatctg 180
aactccctct ctccctggaa taagtatttt tcccacattt ttggatatat gtatggtaga 240
caattttttt ttaagacaca gagataaatg ttttctgtct ttggttacct ttcctttccc 300
ctttaaaagg aattagctat agaactgctt tgtaaagatg cttcttgata ttttactttt 360
gttccctttt cctaactctt cctttttctc cccactctc cagaaggcat aacctttctc 420
tccacacccc ctacccccc ccccgctcta ggtcccatc ctttccatca agaccttcat 480
tagcttatga tatttgcgtc cgagatgtta taacaaggac tcgttcatgt atataagcta 540
tttcttgatc cattttaaag gaattgtaca ttgtgttaga aaaaaaaaaa aaaaaaaaaa 600
aaaaaaaaaa aaaaaaaaaa aaaaa 625

```

<210> 126  
 <211> 24  
 <212> PRT  
 <213> Homo sapiens

<400> 126  
 Met Leu Leu Asp Ile Leu Leu Leu Phe Leu Phe Pro Asn His Ser Leu  
 1 5 10 15  
 Phe Ser Pro Leu Leu Gln Lys Ala  
 20

<210> 127  
 <211> 1946  
 <212> DNA  
 <213> Homo sapiens

<400> 127  
 gaagctgggg ccagcggag gtagcagcag acgcctgaga gcgaggccga ggccccctcag 60  
 ggtttgagaga ccctgacaca cccaccttct caccctgggct ctgcgtatcc cccagccttg 120  
 aggggaagatg aagcctaaac tgatgtacca ggagctgaag gtgcctgcag agggagcccg 180  
 caatgagctg cccatgaatg agattgaggc gtggaaggct gcggaaaaga aagcccgctg 240  
 ggtcctgctg gtcctcatte tggcgggtgt gggcttcgga gccctgatga ctacagctgtt 300  
 tctatgggaa tacggcgact tgcatctctt tgggccccaa cagcgcctcag ccccttgcta 360  
 tgacccttgc gaarcagtgc tgggtggaaa cattcctgar ggcctggact tccccaatgc 420  
 ctccacgggg aacccttcca ccagccaggc ctggctgggc ctgctcgccg gtgcgcacag 480  
 cagcctggac atgcctcct tctactggac cctcaccaac aatgacaccc acacgcagga 540  
 gccctctgac cagcagggtg aggaggtcct ccggcagctg cagaccctgg caccaaaggg 600  
 cgtgaacgtc cgcctcgctg tgagcaagcc cagcggggcc cagccacagc cggacctgca 660  
 ggctctgctg cagagcgggtg cccaggtccg catgggtggac atgcagaagc tgacctatgg 720  
 cgtcctgcat accaagtctt ggggtgggga ccagaccac ttctacctgg gcagtgccaa 780  
 catggactgg cgttccactga cccaggtcaa ggagctgggc gtggctcatgt acaactgcag 840  
 ctgcctggct cgagacctga ccaagatctt tgaggcctac tgggttcctg gccaggcagg 900  
 cagctccatc ccatcaactt ggccccggtt ctatgacacc cgtacaacc aagagacacc 960  
 aatggagatc tgccctcaatg gaaccctgc tctggcctac ctggcgagtg cgccccacc 1020  
 cctgtgtcca agtggccgca ctccagacct gaaggctcta ctcaacgtg tggacaatgc 1080  
 ccggagtctt atctacgtcg ctgtcatgaa ctacctgccc actctggagt tctccaccc 1140  
 tcacaggttc tggcctgcca ttgacgatgg gctgcggcgg gccacctacg agcgtggcgt 1200  
 caaggtgcgc ctgctcatca gctgctgggg acactcggag ccatccatgc gggccttcct 1260  
 gctctctctg gctgccttgc gtgacaacca taccactct gacatccagg tgaaactctt 1320  
 tgtggtcccc gcggatgagg cccaggtcgt aatcccatat gccctgtgta accacaacaa 1380  
 gtacatgggt actgaacgag ccacctacat cggaaacctc aactgggtctg gcaactactt 1440  
 cagggagacg gcgggcacct cgctgctggt gacgcagaat gggaggggag gcctgcggag 1500  
 ccagctggag gccattttcc tgagggactg ggactccct tacagccatg accttgacac 1560  
 ytcagytgac agsgtgggca acgcctgccg cytgytctga ggcccgatcc agtgggcagg 1620  
 ccaaggcctg ctgggcccc gcggaccag gtgytctggg tcacgggtccc tgtccccgca 1680  
 ccccgtytyt tgytygtccc attgtggctc ctcaggytyt ytccccctgt cccccaccty 1740  
 tacctccacc cccaccggcc tgacgctgtg gccccgggac ccagcagagc tggggggagg 1800  
 atcagcccc aaagaaatgg ggggtgcatgc tgggcctggc cccctggccc accccaytt 1860  
 ttcagggcaa aaagggcccc ggggtataat aagtaaataa cttgtctgta aaaaaaaaaa 1920  
 aaaaaaaaaa aaaaaaaaaa aaaaaa 1946

<210> 128  
 <211> 490  
 <212> PRT  
 <213> Homo sapiens

<220>

&lt;221&gt; UNSURE

&lt;222&gt; (83)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (480)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (482)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (490)

&lt;400&gt; 128

Met Lys Pro Lys Leu Met Tyr Gln Glu Leu Lys Val Pro Ala Glu Glu  
 1 5 10 15

Pro Ala Asn Glu Leu Pro Met Asn Glu Ile Glu Ala Trp Lys Ala Ala  
 20 25 30

Glu Lys Lys Ala Arg Trp Val Leu Val Leu Ile Leu Ala Val Val  
 35 40 45

Gly Phe Gly Ala Leu Met Thr Gln Leu Phe Leu Trp Glu Tyr Gly Asp  
 50 55 60

Leu His Leu Phe Gly Pro Asn Gln Arg Pro Ala Pro Cys Tyr Asp Pro  
 65 70 75 80

Cys Glu Xaa Val Leu Val Glu Ser Ile Pro Glu Gly Leu Asp Phe Pro  
 85 90 95

Asn Ala Ser Thr Gly Asn Pro Ser Thr Ser Gln Ala Trp Leu Gly Leu  
 100 105 110

Leu Ala Gly Ala His Ser Ser Leu Asp Ile Ala Ser Phe Tyr Trp Thr  
 115 120 125

Leu Thr Asn Asn Asp Thr His Thr Gln Glu Pro Ser Ala Gln Gln Gly  
 130 135 140

Glu Glu Val Leu Arg Gln Leu Gln Thr Leu Ala Pro Lys Gly Val Asn  
 145 150 155 160

Val Arg Ile Ala Val Ser Lys Pro Ser Gly Pro Gln Pro Gln Ala Asp  
 165 170 175

Leu Gln Ala Leu Leu Gln Ser Gly Ala Gln Val Arg Met Val Asp Met  
 180 185 190

Gln Lys Leu Thr His Gly Val Leu His Thr Lys Phe Trp Val Val Asp  
 195 200 205

Gln Thr His Phe Tyr Leu Gly Ser Ala Asn Met Asp Trp Arg Ser Leu  
 210 215 220

Thr Gln Val Lys Glu Leu Gly Val Val Met Tyr Asn Cys Ser Cys Leu  
 225 230 235 240

Ala Arg Asp Leu Thr Lys Ile Phe Glu Ala Tyr Trp Phe Leu Gly Gln  
 245 250 255

Ala Gly Ser Ser Ile Pro Ser Thr Trp Pro Arg Phe Tyr Asp Thr Arg  
 260 265 270

Tyr Asn Gln Glu Thr Pro Met Glu Ile Cys Leu Asn Gly Thr Pro Ala  
 275 280 285

Leu Ala Tyr Leu Ala Ser Ala Pro Pro Pro Leu Cys Pro Ser Gly Arg  
 290 295 300

Thr Pro Asp Leu Lys Ala Leu Leu Asn Val Val Asp Asn Ala Arg Ser  
 305 310 315 320

Phe Ile Tyr Val Ala Val Met Asn Tyr Leu Pro Thr Leu Glu Phe Ser  
 325 330 335

His Pro His Arg Phe Trp Pro Ala Ile Asp Asp Gly Leu Arg Arg Ala  
 340 345 350

Thr Tyr Glu Arg Gly Val Lys Val Arg Leu Leu Ile Ser Cys Trp Gly  
 355 360 365

His Ser Glu Pro Ser Met Arg Ala Phe Leu Leu Ser Leu Ala Ala Leu  
 370 375 380

Arg Asp Asn His Thr His Ser Asp Ile Gln Val Lys Leu Phe Val Val  
 385 390 395 400

Pro Ala Asp Glu Ala Gln Ala Arg Ile Pro Tyr Ala Arg Val Asn His  
 405 410 415

Asn Lys Tyr Met Val Thr Glu Arg Ala Thr Tyr Ile Gly Thr Ser Asn  
 420 425 430

Trp Ser Gly Asn Tyr Phe Thr Glu Thr Ala Gly Thr Ser Leu Leu Val  
 435 440 445

Thr Gln Asn Gly Arg Gly Gly Leu Arg Ser Gln Leu Glu Ala Ile Phe  
 450 455 460

Leu Arg Asp Trp Asp Ser Pro Tyr Ser His Asp Leu Asp Thr Ser Xaa  
 465 470 475 480

Asp Xaa Val Gly Asn Ala Cys Arg Leu Xaa  
 485 490

&lt;210&gt; 129

&lt;211&gt; 6254

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

agggtcctgg gcagtcgcgc cagagctgag cggaggggcgc ggcgcgagaa cgaatccttg 60  
 tgacattctc tctcagcatt ctttatcccc tgtttgctga agacttcgac caaagctggt 120  
 ctttagctgtt ggcattctcc tgagaaaagg atagcttcag aaatcagaaa aacatttggg 180  
 aggtgtctag cccagtggac cttctgaaga gcaatgctaa gaagacgttt ggtttaaaga 240



attaaaaagga agaacaactt aagagcttct tcaaagtcc ccgcatgaaa attacttaaa 300  
 cggttgcacac aacgtttcac aaaatctttt gtgaaagaag aaaaggaaat tcagtgtgtg 360  
 agtctcagca ggagttaagc taatgcagct taacatcatg ccgacaaaga agcgcttatac 420  
 tgcgggcaga gtgcccctga ttctcttctt gtgccagatg attagtgcac tggaaagtacc 480  
 tcttgatcca aaacttcttg aagacttggt acagcctcca accatcacc aacagtctcc 540  
 aaaagattac attattgacc ctccgggagaa tattgtaatc cagtgtgaag ccaaaggga 600  
 accgccccca agcttttctt ggaccctgaa tgggactcat tttgacatcg ataaagaccc 660  
 tctggtcacc atgaagcctg gcacaggaac gctcataatt aacatcatga gcgaaggga 720  
 agctgagacc tatgaaggag tctatcagtg tacagcaagg aacgaacgag gagctgcagt 780  
 ttctaataac attgttgtcc gcccattccag atcaccattg tggaccaaag aaaaacttga 840  
 accaatcaca cttcaaaagt gtcagttctt agtacttccc tgcagacccc caattggatt 900  
 accaccacct ataataattt ggatggataa ttcttccaa agacttccac aaagtgaag 960  
 agtttctcaa ggtttgaatg gggaccttta tttttccaa gtctctccag aggacacccg 1020  
 cgaagactat atctgttatg ctagatttaa tcatactcaa accatacagc agaagcaacc 1080  
 tatttctgtg aaggtgattt cagctaaatc aagtagagag agggccacca catttttaac 1140  
 tccagaaggc aatgcaagta acaaagagga attaagagga aatgtgcttt cactggagtg 1200  
 cattgcagaa ggactgccta ccccaattat ttactgggca aaggaaagtg gaatgctacc 1260  
 caaaaaacag acagtttata agaactttga gaaaaccttg cagatcattc atgtttcaga 1320  
 agcagactct ggaaattacc aatgtatagc aaaaaatgca ttaggagcca tccaccatac 1380  
 catttctgtt agagttaaag cggctccata ctggatcaca gcccctcaaa atcttctgtt 1440  
 gtccccagga gaggatggga ccttgatctg cagagctaatt ggcaacccca aaccagaat 1500  
 tagctggtta acaaatggag tcccaataga aattgcccc gatgacccca gcagaaaaat 1560  
 agatggcgat accattattt ttcaaatgt tcaagaaaga tcaagtgcag tatatcagt 1620  
 caatgcctct aatgaatatg gatatttact ggcaaacgca ttgttaaatg tgctggctga 1680  
 gccaccacga atctctcac ctgcaaacac actctaccag gtcattgcaa acaggcctgc 1740  
 ttacttagac tgtgcttctt ttgygtctcc tctcccaacc atcgagtggg ttaaaggagc 1800  
 taaaggaagt gctcttcatg aagatattta tgttttacat gaaaatggaa ctttggaat 1860  
 tctgtgggccc caaaaggaca gtacaggaac ttatacgtgt gttgcaagga ataaattag 1920  
 gatggcaaa aatgaagttc acttagaaat caaagatgct acatggatcg ttaaacagcc 1980  
 cgaatatgca gttgtgcaaa gagggagcat ggtgtctctt gaatgcaaa tgaaacatga 2040  
 tcacacctta tccctcactg tctgtgggct gaaggacaac agggaaactgc ccagtgtatga 2100  
 aaggttccat gttgacaagg atcatctagt ggtagctgat gtcagtgcag atgacagcgg 2160  
 gacctacacg tgtgtggcca acaccactct ggacagcgtc tccgccagcg ctgtgcttag 2220  
 cgttgttgc tctactccaa ctccagctcc cgtttacgat gtcccaaatc ctccctttga 2280  
 cttagaactg acagatcaac ttgacaaaag tgttcagctg tcatggacc caggcgatga 2340  
 caacaatagc ccattacaa aattcatcat cgaatatgaa gatgcaatgc acaagccagg 2400  
 gctgtggcac caccaaactg aagtttcttg aacacagacc acagcccagc tgaagctgtc 2460  
 tcttactctg aactactcct tccgcgtgat ggcagtgaac agcattggga agagcttgcc 2520  
 cagcgaggcc tctgagcagt atttgacgaa agcctcagaa ccagataaaa accccacagc 2580  
 tgtggaagga ctgggatcag agcctgataa tttgttgatt acgtggaagc ccttgaatgg 2640  
 tttcgaatct aatgggcccag gccttcagta caaagttagc tggcgccaga aagatggtga 2700  
 tgaatgaatg acatctgttg ttgtggcaaa tgtatccaaa tatattgtct caggcacgcc 2760  
 aacctttgtt ccatacctga tcaaagtcca ggcctgaat gacatggggt ttgccccga 2820  
 gccagctgta gtcattgggac attctggaga agacctccca atggtggctc ctgggaacgt 2880  
 gcgtgtgaat gtggtgaaca gtaccttagc cgaggtgcac tgggaccag tacctctgaa 2940  
 aagcatccga ggacacctac aaggctatcg gatttactat tgggaagacc agagttcatc 3000  
 taaaagaaac agacgtcaca ttgagaaaa gatcctcacc ttccaaggca gcaagactca 3060  
 tggcatgttg ccggggctag agccctttag ccactacaca ctgaatgtcc gagtgtcaa 3120  
 tgggaaaggg gagggcccag ccagccctga cagagtcttt aatactccag aaggagtccc 3180  
 cagtgtcccc tcttctttga agattgtgaa tccaacactg gactctctca ctttggatg 3240  
 ggatccaccg agccaccgga atggcatttt gacagagtac acctaaagt atcagccaat 3300  
 taacagcaca catgaattag gccctctggt agatttgaat attcctgcca acaagacagc 3360  
 gtggacttta aaaaatttaa atttcagcac tcgatataag ttttattttt atgcacaaac 3420  
 atcagcagga tcaggaagtc aaattacaga ggaagcagta acaactgttg atgaagctgg 3480  
 tattcttcca cctgatgtag gtgcaggcaa agcagtgcca agccggcagg tggatattgc 3540  
 aactcagggc tgggttcattg gtctgatgtg tgcgttgct ctccttatct taattttgct 3600  
 gattgtttgc ttcacagaa gaaacaaggg tggtaaatat ccagttaaag aaaagggaaga 3660  
 tgcccatgct gacctgaaa tccagcctat gaaggagat gatgggacat ttggagaata 3720  
 cagtgtgca gaagaccaca agcctttgaa aaaagggaag cgaactcctt cagacaggac 3780  
 tgtgaaaaaa gaagatagtg acgacagcct agttgactat ggagaagggg ttaattggcca 3840

```

gttcaatgag gatggctcct ttattggaca atacagtggg aagaaagaga aagagccggc 3900
tgaaggaaac gaaagctcag aggcaccttc tctgtcaac gccatgaatt cctttgttta 3960
atthttaagc tctttgccaa tattccattt ctctagaatg tttatcctaa gcacttgttt 4020
gtcagccctc tcatactatg aacatatggg tagagagtat attttctgct gtatgttagt 4080
attatgagaa tagttacagc aaaaacataa ctcagtcaaa tgatatgtta atatgaactg 4140
gaatgcaaag tgcatacttt ttcattcaaa atgggtattc ttgatttcct cagaactgat 4200
aaaaataat gcaacatcac caacagatcc tgttatttcc tctgcaggat acagtccaat 4260
atgatgcag aaaaatgctc cacatttaaa ggacataccc gtgtatgtta tgaaaacatg 4320
gtttgatact ttgtttatc taccctcagc tgaaccctta tatatgaatt ccgttttcat 4380
tgtcaagaat gttactgtag tattctctag aacttcaatg tctttgtgga cattgttggtg 4440
aaattgggtg ctatgtatag ctgtcgttag tctttttggg agactgttag gaacagtgtg 4500
tacagtatat acttgctaaa tgagttcatt atgacagtca cattgtctga gcttactgag 4560
aactattacc tactcttggc tctgttact ccgtaggctt cttaatcttc caggcattac 4620
agcagcacag tgttctactt tttacatcat ttctatgttc ggttgttttt aggcataaac 4680
aatgtgtatt gcagtgcatt tcggcatttg tgccatactg aaagaatcaa aaacaaatca 4740
tccaaatcaa atttcaaaca ttatttcaga gaacacaggg caagacacat acagtgcctt 4800
cagatattaa gcattccaca acatcgtgca ttctgtatca gctgggccag tccattctgg 4860
gtcctagatt actgtcattg tctaaaagta acttttaaaa agcagagtgc atgaaaactg 4920
caatgctggg aaaaagaagga aacatgaaaa taaaaataag acagtttatt agaaatagca 4980
tttctcata agcataaaaa gaaatctttg ttgccaactg aagcacatgg gattttgtgg 5040
tcttttatgg ttctcataac attcagtaag aaagatgtca acatgctaga aaattaattt 5100
taaaactaag ttattccaac actaaaagca tacaacagca tgccaacagt aatatattat 5160
tctccaagac ttacctatg taagtgttca aaactctgca gcattaaaca acgtgtatgc 5220
aaattgttat ggatacattt cagaatctaa gaaatcaggc aagtgtctaa aaggccaacg 5280
gtccaaggga ttacatctgc agtttaaaaa gtaaatatat attctatcgt attcataaac 5340
aatactatc aaatgggtta cctccaaata tgaaaatcta taacaaccta tgggtgaagg 5400
aatgctcagc ttcatctgac aataaattgg tttctcataa cttgcacaa gtttaatttt 5460
aagtaaagct ttttatatgt agatattttg ttgaatttgt aaatacactt aaaatgtaga 5520
tgctatatgc ttatagggtg tacatacaaa taaacatgca atgtttatgt tgaactgtat 5580
aagaggtaag ctaattaatg cagtgaatgg gattggaaag catctactta aatatctatt 5640
gggttcccc cttccccac cttttttgct gtgaaactga aatagtgaac ttttctacgt 5700
attgacagca gatttttcga tgaaatcttc agagctttgc ctatggggca cagtaggcct 5760
agtaacctgg catgtttgat atatgtagg aaagcataat ttaaagtaat ccaggtaaa 5820
gatggcccta aatactttca tgtctctata ttcatttttc acagatccac ctgtctcttg 5880
aaaatataaa aagacaaaac aggtttgcct tggcatcaga gagcacaag attaaaagtt 5940
actttaaatt tgccaatatt ttgggagaac aataaaaacta cattttttcy tyttccatac 6000
tggtagatgc gaaatttatc tgtgcatgaa agggtcactt ctgtaatagt gcacagattt 6060
ggtattaaaa attaaatgtg gttttaaaaa ttcctytytc ttttgtaatt tatgtcccca 6120
attgagtgtg aatgtccaag taattggtga tgtaaatgga caggcaaatg tgactggatt 6180
tccctcaaaa aagtaactat taaacagtyt tgatctcaaa aaaaaaaaaa aaaaaaaaaa 6240
aaaaaaaaaa aaaa 6254

```

&lt;210&gt; 130

&lt;211&gt; 1192

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

```

Met Gln Leu Asn Ile Met Pro Thr Lys Lys Arg Leu Ser Ala Gly Arg
  1                      5                      10                     15

```

```

Val Pro Leu Ile Leu Phe Leu Cys Gln Met Ile Ser Ala Leu Glu Val
      20                      25                      30

```

```

Pro Leu Asp Pro Lys Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile
      35                      40                      45

```

```

Thr Gln Gln Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile
      50                      55                      60

```

Val Ile Gln Cys Glu Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp  
 65 70 75 80  
 Thr Arg Asn Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr  
 85 90 95  
 Met Lys Pro Gly Thr Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly  
 100 105 110  
 Lys Ala Glu Thr Tyr Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu  
 115 120 125  
 Arg Gly Ala Ala Val Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser  
 130 135 140  
 Pro Leu Trp Thr Lys Glu Lys Leu Glu Pro Ile Thr Leu Gln Ser Gly  
 145 150 155 160  
 Gln Ser Leu Val Leu Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro  
 165 170 175  
 Ile Ile Phe Trp Met Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu  
 180 185 190  
 Arg Val Ser Gln Gly Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu  
 195 200 205  
 Pro Glu Asp Thr Arg Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His  
 210 215 220  
 Thr Gln Thr Ile Gln Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser  
 225 230 235 240  
 Ala Lys Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly  
 245 250 255  
 Asn Ala Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu  
 260 265 270  
 Cys Ile Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu  
 275 280 285  
 Asp Gly Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn Phe Glu Lys  
 290 295 300  
 Thr Leu Gln Ile Ile His Val Ser Glu Ala Asp Ser Gly Asn Tyr Gln  
 305 310 315 320  
 Cys Ile Ala Lys Asn Ala Leu Gly Ala Ile His His Thr Ile Ser Val  
 325 330 335  
 Arg Val Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln Asn Leu Val  
 340 345 350  
 Leu Ser Pro Gly Glu Asp Gly Thr Leu Ile Cys Arg Ala Asn Gly Asn  
 355 360 365  
 Pro Lys Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro Ile Glu Ile  
 370 375 380

Ala Pro Asp Asp Pro Ser Arg Lys Ile Asp Gly Asp Thr Ile Ile Phe  
 385 390 395 400  
 Ser Asn Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser  
 405 410 415  
 Asn Glu Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala  
 420 425 430  
 Glu Pro Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr Gln Val Ile  
 435 440 445  
 Ala Asn Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu  
 450 455 460  
 Pro Thr Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu  
 465 470 475 480  
 Asp Ile Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Pro Val Ala  
 485 490 495  
 Gln Lys Asp Ser Thr Gly Thr Tyr Thr Cys Val Ala Arg Asn Lys Leu  
 500 505 510  
 Gly Met Ala Lys Asn Glu Val His Leu Glu Ile Lys Asp Ala Thr Trp  
 515 520 525  
 Ile Val Lys Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val  
 530 535 540  
 Ser Phe Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val  
 545 550 555 560  
 Leu Trp Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr  
 565 570 575  
 Val Asp Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser  
 580 585 590  
 Gly Thr Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala  
 595 600 605  
 Ser Ala Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro Ala Pro Val  
 610 615 620  
 Tyr Asp Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu  
 625 630 635 640  
 Asp Lys Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser  
 645 650 655  
 Pro Ile Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro  
 660 665 670  
 Gly Leu Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala  
 675 680 685  
 Gln Leu Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala  
 690 695 700

Val Asn Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr  
 705 710 715 720  
 Leu Thr Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly  
 725 730 735  
 Leu Gly Ser Glu Pro Asp Asn Leu Val Ile Thr Trp Lys Pro Leu Asn  
 740 745 750  
 Gly Phe Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg  
 755 760 765  
 Gln Lys Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val  
 770 775 780  
 Ser Lys Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile  
 785 790 795 800  
 Lys Val Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val  
 805 810 815  
 Val Met Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn  
 820 825 830  
 Val Arg Val Asn Val Val Asn Ser Thr Leu Ala Glu Val His Trp Asp  
 835 840 845  
 Pro Val Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile  
 850 855 860  
 Tyr Tyr Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg Arg His Ile  
 865 870 875 880  
 Glu Lys Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu  
 885 890 895  
 Pro Gly Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val  
 900 905 910  
 Asn Gly Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr  
 915 920 925  
 Pro Glu Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro  
 930 935 940  
 Thr Leu Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn  
 945 950 955 960  
 Gly Ile Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr  
 965 970 975  
 His Glu Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr  
 980 985 990  
 Arg Trp Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr  
 995 1000 1005  
 Phe Tyr Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu  
 1010 1015 1020

Ala Val Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly  
1025 1030 1035 1040

Ala Gly Lys Ala Met Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly  
1045 1050 1055

Trp Phe Ile Gly Leu Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu  
1060 1065 1070

Leu Ile Val Cys Phe Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val  
1075 1080 1085

Lys Glu Lys Glu Asp Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys  
1090 1095 1100

Glu Asp Asp Gly Thr Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys  
1105 1110 1115 1120

Pro Leu Lys Lys Gly Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys  
1125 1130 1135

Glu Asp Ser Asp Asp Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly  
1140 1145 1150

Gln Phe Asn Glu Asp Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys  
1155 1160 1165

Glu Lys Glu Pro Ala Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro  
1170 1175 1180

Val Asn Ala Met Asn Ser Phe Val  
1185 1190

<210> 131

<211> 4253

<212> DNA

<213> Homo sapiens

<400> 131

gcgatcagaa gactgaggca gtgctgcagg tgaacatggc tgtagcctac caatccttca 60  
ttttggctga cttcataatt gaacctgctc actgccaccc agtcgttcac atggcaaac 120  
ccagtgttcc ttaagtgggc tgaaaagaat ggaatcctag acctgtcttg ttagagtara 180  
agctcattga gctgcctgcc cttccatatt gcttgtggac ctatgaatgg tgctctttaa 240  
aatgtcagtg tagagggact gggaaatcctg tattcctgcc ctatcattct gtaactttga 300  
gaagcatgtg ggctcagtg aractactta ttttagttc tgttagaaca ggatttttaa 360  
gaaacctatc gaacagaaga aataaagcgg aaggttaagct cagctcatgt gccatcaag 420  
ctgcataaat ctccatctgc tctgggaaac attcatggga acagaaggat tcttcttctc 480  
gagaatgttg ttttcattat ataactatag atacagcatg tgggtgattt ctgtgtacaa 540  
atactttacc catgagaaat gtatagctgt tagatatgtg tgggctcaca catatatgca 600  
atagatgcta tacatagcga tgtgcatgtg tatttgtata tatttatgtt catattttaa 660  
catatgaaac atgaaataga agtataatat tatttttcta tccaaatagt taacagagca 720  
gatgccctta gattctaata tgttgttcag tcctgaagat agccaagtta aatataaaaa 780  
caggagaaga gaaaaataa aaktccattg agaaggaata gagagaaaga acrggtcttg 840  
tgaatgagaa kttcatttgg atcaacacag catttcctar aatgagtctg cactgtgctt 900  
tttgcarara craatgggct ccttaggctc tccacggctt ttgatggcar atgaktgttc 960  
tctgtttcar atgaktcaag ctccagctct ggaaggcaga tgctcctcct cgatggtggg 1020  
ccaccgggcc agtcaracac agacagctcc cgtggaggag agcgacttgc acaccatgcc 1080  
agacattgag agtgataaaa acatcatccg gaccaagatg ttcctttacc tgtcagattt 1140  
gtccagggaag gaccggagaa ttgtcagcaa aaaatataaa atttattttt ggaacatcat 1200

```

caccattgct gtgttttacg cgctgcccgat gccagctg gtcattacct atcagacagt 1260
ggtaaatgtc actggcaacc aggacatctg ttactacaac ttcctctgtg ctcacccctt 1320
gggcgtcctg agtgccttca acaacattct cagcaatctg ggccacgtgc ttcctgggctt 1380
cctcttcctg ctgatatgtc tgcgccgca catcctccat cggagagccc tggaaagcaa 1440
ggacatcttt gctgtggagt acgggattcc caaacacttt ggtctcttct acgctatggg 1500
cattgcattg atgatggaag ggggtgctag tgcctgtctc catgtctgcc ctaattatcc 1560
caacttccaa ttcgacacct ccttcattga catgatcgct gccctgtgca tgcgaaagct 1620
ctatcagacc cgccaccag acatcaatgc cagcgctac tctgcctatg cctcctttgc 1680
tgtggctcatc atggctcaccg tccttgaggt ggtgtttgga aaaaatgacg tatggttctg 1740
ggtcattctt tctgcaatcc acgttctggc ctgcctagcc ctcagcacc aaatatatta 1800
tatgggtcgt tcaagatag atgtgtctga cacagatttg ggaattttcc ggcgggctgc 1860
catgggtgtc tacacagact gtatccagca gtgtagccga cctctatata tggatagaat 1920
gggtgtgctg gttgtgggga atctggttaa ctggtccttc gccctctttg gattgatata 1980
ccgccccagg gaactttgctt cctacatgct gggcatcttc atctgtaacc ttttgcgtga 2040
cctggccttt tacatcatca tgaagctccg cagctctgaa aaggctctcc cagtcccgtc 2100
cttctgcacc gtggccaccg ctgtgatgtg ggctgcccgc ctatattttt tcttcagaa 2160
tctcagcagc tgggagggaa ctccggccga atccgggag aagaaccgcg agtgcattct 2220
gctggatttc ttcgatgacc atgacatctg gcacttctc tctgctactg ctctgttttt 2280
ctcattcttg gttttgttaa ctttgatga tgacctgat gtggttcgga gagaccagat 2340
ccctgtcttc tgaacctcca acattaagag aggggaggga gcgatcaatc ttgggtgctg 2400
ttcacaaaaa ttacagtac cacagcaaa taaccactgc cagatgctcc actcaccctc 2460
ttagagacca actctgcatt cacacaggaa ggagaggggc tgcgggagat ttaaaccctg 2520
aagaaaggag gcagaaggag agccatgttt tgaggacaga cgaaccctg aggagctgag 2580
aaacacttgc tcttccatc tgcagctttg ggagtgcac agggataggc actgcacca 2640
agtcaactca ccatcttggg gtccctccca cctcacgga gactgcccag caatggcaga 2700
atgctgtgct acacttccct ccagttgtca cctgcccag aaaggccagc agcttgga 2760
tcttgcccag aaactgtgtt ggcccccttc acacctctgc aacacctgct gctccagcaa 2820
gaggatgtga tcttttagaa tatggcgggg aggtgacccc aggcctgccc ctactgggat 2880
agatgtttta atggcaccag ctagtccact ccagaagaa actctgtata tttcccccag 2940
gtttctgatg ccatcagaag ggctcaggag tgggggttct cacacattcc tcttaacaag 3000
taactgtcac tgggaccgag tctgggtgct ttacatattc cttcgtgtct tcactcact 3060
gacctgtgtg gacctcatca ctctgactct gccttcttgg aaaggccctg tcaactccaca 3120
gatgtctggc cagcttcaag gcagaaggaa aaacaggaaa agctctttta acagcagcag 3180
gaacaagaga aatgactaac catactaaaa gactggtaac agcagcagca gccagacagg 3240
cctcacctta aggacttggg ctgccagagc aaattcagca gagcttattt ggcctcccat 3300
tcacacagct cagttctgtg cccacatcac ctttggggaa gaaatcagca tctaatcag 3360
ggacactact tcaggagtcc tccacagcga gtccgtcatc tgcacttta ttagatcag 3420
ggttctagac tcttccctg aggttctcag aagcagctct caggatgaac gtattgtcct 3480
cttccctctc tcttgcaaa tgacagcta atctaattgt gtctctcggt tgcacctgac 3540
attctctccc cagtaagggt ttggcaagct cagcatctgg gttccactct cacactgtct 3600
ggcagctctg tgtctgagaa gttctacatt gaccaggccc cttgttgcc tggagtatga 3660
cgtaaatcaga aaatagacgt ataaatgtgc acatgcgtat gtatttgctt gtgaaattaa 3720
agtcacctct tgcctctgct tctctgatca ttcgttagag aaatggatca ggcatttttt 3780
taaattatta tcttttctct aaactatttg cattgtgttc aaaaacccat tttagaagtt 3840
tgaacagcaa gcttttctct attttaaaaa cacaaagttg ctttcaatga aatattttgt 3900
gattttttta aagtccccaa atgtgtactt agccttctgt tattccttat tctttaagca 3960
gtgttggtct ccattgacca tatgaaggcc accaattaaa tgggtgtgtt aatccaacat 4020
gtaaaaaact ttttggcagg gcacagtggc tcacgcctgt aatcccaaca ctttgggagg 4080
ctgaggcagg aggatcamtt gagcccagga gattgacgcc gcagtgaact atgattgtgc 4140
ccctgcactc cagcctggat gacagagtga gaccccatyt yttaaaaaat aaaaaaaat 4200
aaaaatttga acctgtttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 4253

```

&lt;210&gt; 132

&lt;211&gt; 479

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (13)..(14)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (21)

&lt;400&gt; 132

Met Gly Ser Val Gly Ser Pro Arg Leu Leu Met Ala Xaa Xaa Leu Ser  
 1 5 10 15

Leu Phe Gln Met Xaa Gln Ala Pro Val Leu Glu Gly Arg Cys Pro Pro  
 20 25 30

Pro Met Val Gly His Arg Ala Ser Gln Thr Gln Thr Ala Pro Val Glu  
 35 40 45

Glu Ser Asp Phe Asp Thr Met Pro Asp Ile Glu Ser Asp Lys Asn Ile  
 50 55 60

Ile Arg Thr Lys Met Phe Leu Tyr Leu Ser Asp Leu Ser Arg Lys Asp  
 65 70 75 80

Arg Arg Ile Val Ser Lys Lys Tyr Lys Ile Tyr Phe Trp Asn Ile Ile  
 85 90 95

Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Ile Gln Leu Val Ile Thr  
 100 105 110

Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr  
 115 120 125

Asn Phe Leu Cys Ala His Pro Leu Gly Val Leu Ser Ala Phe Asn Asn  
 130 135 140

Ile Leu Ser Asn Leu Gly His Val Leu Leu Gly Phe Leu Phe Leu Leu  
 145 150 155 160

Ile Val Leu Arg Arg Asp Ile Leu His Arg Arg Ala Leu Glu Ala Lys  
 165 170 175

Asp Ile Phe Ala Val Glu Tyr Gly Ile Pro Lys His Phe Gly Leu Phe  
 180 185 190

Tyr Ala Met Gly Ile Ala Leu Met Met Glu Gly Val Leu Ser Ala Cys  
 195 200 205

Tyr His Val Cys Pro Asn Tyr Ser Asn Phe Gln Phe Asp Thr Ser Phe  
 210 215 220

Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Thr Arg  
 225 230 235 240

His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Ser Phe Ala  
 245 250 255

Val Val Ile Met Val Thr Val Leu Gly Val Val Phe Gly Lys Asn Asp  
 260 265 270

Val Trp Phe Trp Val Ile Phe Ser Ala Ile His Val Leu Ala Ser Leu  
 275 280 285



Ala Leu Ser Thr Gln Ile Tyr Tyr Met Gly Arg Phe Lys Ile Asp Val  
 290 295 300

Ser Asp Thr Asp Leu Gly Ile Phe Arg Arg Ala Ala Met Val Phe Tyr  
 305 310 315 320

Thr Asp Cys Ile Gln Gln Cys Ser Arg Pro Leu Tyr Met Asp Arg Met  
 325 330 335

Val Leu Leu Val Val Gly Asn Leu Val Asn Trp Ser Phe Ala Leu Phe  
 340 345 350

Gly Leu Ile Tyr Arg Pro Arg Asp Phe Ala Ser Tyr Met Leu Gly Ile  
 355 360 365

Phe Ile Cys Asn Leu Leu Leu Tyr Leu Ala Phe Tyr Ile Ile Met Lys  
 370 375 380

Leu Arg Ser Ser Glu Lys Val Leu Pro Val Pro Leu Phe Cys Ile Val  
 385 390 395 400

Ala Thr Ala Val Met Trp Ala Ala Ala Leu Tyr Phe Phe Phe Gln Asn  
 405 410 415

Leu Ser Ser Trp Glu Gly Thr Pro Ala Glu Ser Arg Glu Lys Asn Arg  
 420 425 430

Glu Cys Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe  
 435 440 445

Leu Ser Ala Thr Ala Leu Phe Phe Ser Phe Leu Val Leu Leu Thr Leu  
 450 455 460

Asp Asp Asp Leu Asp Val Val Arg Arg Asp Gln Ile Pro Val Phe  
 465 470 475

<210> 133  
 <211> 462  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
 gtggaaggag tggataataa aatgagtcag tgcaccagct ccaccattcc tagctcaagt 60  
 caagagaaag accctaaaat taagacagag acaagtgaag agggatctgg agacttggat 120  
 aatctagatg ctattcttgg tgatctgact agttctgact ttacaataa ttccatatcc 180  
 tcaaatggta gtcactctgg gactaagcaa caggtgtttc aaggaactaa ttctctgggt 240  
 ttgaaaagtt cacagtcctgt gcagtcctatt cgctctccat ataaccgagc agtgtctctg 300  
 gatagccctg tttctgttgg ctcaagtcct ccagtaaaaa atatcagtcg tttcccatg 360  
 ttaccaaagc aacccatgtt ggggtgggaat ccaagaatga tggatagtca rgaaaattat 420  
 ggctcaagta tgggagactg gggcttacca aactcaaagg cc 462

<210> 134  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
 Met Ser Gln Cys Thr Ser Ser Thr Ile Pro Ser Ser Ser Gln Glu Lys  
 1 5 10 15

Asp Pro Lys Ile Lys Thr Glu Thr Ser Glu Glu Gly Ser Gly Asp Leu  
20 25 30

Asp Asn Leu Asp Ala Ile Leu Gly Asp Leu Thr Ser Ser Asp Phe Tyr  
35 40 45

Asn Asn Ser Ile Ser Ser Asn Gly Ser His Leu Gly Thr Lys Gln Gln  
50 55 60

Val Phe Gln Gly Thr Asn Ser Leu Gly Leu Lys Ser Ser Gln Ser Val  
65 70 75 80

Gln Ser Ile Arg Pro Pro Tyr Asn Arg Ala Val Ser Leu Asp Ser Pro  
85 90 95

Val Ser Val Gly Ser Ser Pro Pro Val Lys Asn Ile Ser Ala Phe Pro  
100 105 110

Met Leu Pro Lys Gln Pro Met Leu Gly Gly Asn Pro Arg Met Met Asp  
115 120 125

Ser Gln Glu Asn Tyr Gly Ser Ser Met Gly Asp Trp Gly Leu Pro Asn  
130 135 140

Ser Lys Ala  
145

<210> 135  
<211> 119  
<212> DNA  
<213> Homo sapiens

<400> 135  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 119

<210> 136  
<211> 3316  
<212> DNA  
<213> Homo sapiens

<400> 136  
ggtaagatgg cggctgtgag tctgcggctc ggcgacttgg tgtgggggaa actcggccga 60  
tatcttcctt ggccaggaaa gattgttaat ccaccaagg acttgaagaa acctcgcgga 120  
aagaaatgct tctttgtgaa attttttggg acagaagatc atgcctggat caaagtggaa 180  
cagctgaagc catatcatgc tcataaagag gaaatgataa aaattaacaa gggtaaacga 240  
ttccagcaag cggtagatgc tgtcgaagag ttcttcagga gagccaaagg gaaagaccag 300  
acgtcatccc acaattcttc tgatgacaag aatcgacgta attccagtga ggagagaagt 360  
aggccaaact cagggtgatga gaagcgcaaa cttagcctgt ctgaagggaa ggtgaagaag 420  
aacatgggag aaggaaagaa gaggggtgtc tcaggctctt cagagagagg ctccaaatcc 480  
cctctgaaaa gagcccaaga gcaaaagtc cgggaagcggg gtcggccccc aaaggatgag 540  
aaggatctca ccatcccggg gtctagtacc gtgaagggga tgatggccgg accgatggcc 600  
gcgtttaaat ggcagccaac cgcaagcgag cctgttaaag atgcagatcc tcatttccat 660  
catttcctgc taagccaaac agagaagcca gctgtctgtt accaggcaat cacgaagaag 720  
ttgaaaatat gtgaagagga aactggctcc acctccatcc aggcagctga cagcacagcc 780  
gtgaatggca gcatcacacc cacagacaaa aagataggat ttttgggcct tgggtctcatg 840  
ggaagtggaa tcgtctccaa cttgctaaaa atgggtcaca cagtgtactgt ctggaaccgc 900  
actgcagaga aagagggggc ccgtctggga agaaccctcg ctgaagtctg ctcaacctgc 960

```

gacatcactt tcgcctgcgt gtcggatccc aaggcggcca aggacctggt gctggggccc 1020
agtgggtgtc tgcaagggat ccgccctggg aagtgtctacg tggacatgtc aacagtggac 1080
gctgacaccg tcaactgagct ggcccagggt attgtgtcca ggggggggcg ctttctggaa 1140
gcccccgctc cagggaatca gcagctgtct aatgacggga tgttggtgat cttagcggct 1200
ggagacaggg gcttatatga ggactgcagc agctgcttcc aggcgatggg gaagacctcc 1260
ttcttctctag gtgaagtggg caatgcagcc aagatgatgc tgatcgtgaa catggtccaa 1320
gggagcttca tggccactat tgccgagggg ctgaccctgg ccaggtgac aggccagtcc 1380
cagcagacac tcttgacat cctcaatcag ggacagttag ccagatctt cctggaccag 1440
aagtgcacaa atatcctgca aggaaacttt aagcctgatt tctacctgaa atacattcag 1500
aaggatctcc gcttagccat tgcgctgggt gatgcggtca accatccgac tcccatggca 1560
gctgcagcaa atgaggtgta caaaagagcc aaggcgctgg accagtctga caacgatatg 1620
tccgcgctgt accgagccta catacactaa gctgtcgaca ccccgccctc acccctccaa 1680
tccccctctc gacccctctc tcttcacatg ggttcggggg cctgggagtt cattctggac 1740
cagccacact atctccatct ccttttatac agactttgag acttgccatc agcacagcac 1800
acagcagcac ctttccctcg aggcgggtgg ggaggggaca agtgtcagca ggattggcgt 1860
gtgggaaagc tcttgagctg ggcactggcc ccccgagcga ggtggctgtg tgttcacaca 1920
cacacacaca cacacacaca cacaggctct cgccccagga tagaagctgc ccagaaactg 1980
ctgcctggct ttttttcttc cgagcttctc ttatctcaaa ccccttccag tcaaggaaact 2040
agaatcagca acgagagttg gaagccttcc cacagcttcc ccagagcga agaggctgta 2100
gtcatgtccc catccccac tggattccct acaaggagag gccttgggccc cagatgagcc 2160
agtacagact ccagacagag gggcccttgg ggccttccaa cctcaggtga tgagctgaga 2220
aagatgttca cgtctaagcg tccagtgtgc acccagcgct ccatagacgc ctttgtgaac 2280
tgaaaagaga ctggcagagt cccgagaaga tggggccctg gctttccagg gagtgcagca 2340
agcagccggc ctgcagaccc agcctgacca acgatgagca tttcttaggc tcagctcttg 2400
atacggaaac gagtgtcttc actccagcca gcatcatggt cttcgggtgt tcccgggccc 2460
ggggtctgtc gggagggaaag agaaactggg ctgacctacc tgaactgact ggccttccga 2520
ggtgggtctg ggacatccta gaggccttac atttgcctt ggatagggga ccgggggggg 2580
cttggaaatg tgcaaaaaaa aaagttaccc aagggatgtc agttttttat cctctgcat 2640
gggttggtat ttccaaaatc ataatttgca gaagggaagg cagcatctac gatgcaatat 2700
gtaattatat atagggtggc cacactaggg cggggctcct ccccccctac agctttggcc 2760
cctttcagag attagaaact ggggttagagg attgcagaag acgagtgggg ggagggcagg 2820
gaagatgcct gtcgggtttt tagcacagtt catttctact ggattttgaa gcatttctgt 2880
ctggacacaa agcctgttct agtcttggcg gaacacactg ggggtggggg cggggggaaga 2940
tgcggtaatg aaaccggtta gtcaattttg tcttaatat gttgacaatt ctgtaaagt 3000
cctttttatg aatatttctg tttaagctat ttcacctttc ttttgaaatc cttccctttt 3060
aaggagaaaa tgtgacactt gtgaaaaagc ttgtaagaaa gcccctccct tttttcttta 3120
aacctttaaa tgacaaatct aggtaatata ggttgtgaat ttttattttt gctttgtttt 3180
taatgaacat ttgtctttca gaataggatt gtgtgataat gtttaaatgg caaaaacaaa 3240
acatgatttt gtgcaattaa caaagctact gcaagaaaaa taaaacactt cttggttaaca 3300
caaaaaaaaa aaaaaa 3316

```

&lt;210&gt; 137

&lt;211&gt; 547

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

```

Met Ala Ala Val Ser Leu Arg Leu Gly Asp Leu Val Trp Gly Lys Leu
  1              5              10              15

Gly Arg Tyr Pro Pro Trp Pro Gly Lys Ile Val Asn Pro Pro Lys Asp
          20              25              30

Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly
          35              40              45

Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His
          50              55              60

Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln

```

65	70	75	80
Gln Ala Val Asp	Ala Val Glu Glu Phe	Leu Arg Arg Ala Lys Gly Lys	
	85	90	95
Asp Gln Thr Ser	Ser His Asn Ser	Ser Asp Asp Lys Asn Arg Arg Asn	
	100	105	110
Ser Ser Glu Glu Arg	Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys		
	115	120	125
Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys			
	130	135	140
Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu			
	145	150	155
Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys			
	165	170	175
Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met			
	180	185	190
Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu			
	195	200	205
Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln			
	210	215	220
Thr Glu Lys Pro Ala Val Cys Tyr Gln Ala Ile Thr Lys Lys Leu Lys			
	225	230	235
Ile Cys Glu Glu Glu Thr Gly Ser Thr Ser Ile Gln Ala Ala Asp Ser			
	245	250	255
Thr Ala Val Asn Gly Ser Ile Thr Pro Thr Asp Lys Lys Ile Gly Phe			
	260	265	270
Leu Gly Leu Gly Leu Met Gly Ser Gly Ile Val Ser Asn Leu Leu Lys			
	275	280	285
Met Gly His Thr Val Thr Val Trp Asn Arg Thr Ala Glu Lys Glu Gly			
	290	295	300
Ala Arg Leu Gly Arg Thr Pro Ala Glu Val Val Ser Thr Cys Asp Ile			
	305	310	315
Thr Phe Ala Cys Val Ser Asp Pro Lys Ala Ala Lys Asp Leu Val Leu			
	325	330	335
Gly Pro Ser Gly Val Leu Gln Gly Ile Arg Pro Gly Lys Cys Tyr Val			
	340	345	350
Asp Met Ser Thr Val Asp Ala Asp Thr Val Thr Glu Leu Ala Gln Val			
	355	360	365
Ile Val Ser Arg Gly Gly Arg Phe Leu Glu Ala Pro Val Ser Gly Asn			
	370	375	380
Gln Gln Leu Ser Asn Asp Gly Met Leu Val Ile Leu Ala Ala Gly Asp			

385                      390                      395                      400  
 Arg Gly Leu Tyr Glu Asp Cys Ser Ser Cys Phe Gln Ala Met Gly Lys  
                          405                      410                      415  
 Thr Ser Phe Phe Leu Gly Glu Val Gly Asn Ala Ala Lys Met Met Leu  
                          420                      425                      430  
 Ile Val Asn Met Val Gln Gly Ser Phe Met Ala Thr Ile Ala Glu Gly  
                          435                      440                      445  
 Leu Thr Leu Ala Gln Val Thr Gly Gln Ser Gln Gln Thr Leu Leu Asp  
                          450                      455                      460  
 Ile Leu Asn Gln Gly Gln Leu Ala Ser Ile Phe Leu Asp Gln Lys Cys  
                          465                      470                      475                      480  
 Gln Asn Ile Leu Gln Gly Asn Phe Lys Pro Asp Phe Tyr Leu Lys Tyr  
                          485                      490                      495  
 Ile Gln Lys Asp Leu Arg Leu Ala Ile Ala Leu Gly Asp Ala Val Asn  
                          500                      505                      510  
 His Pro Thr Pro Met Ala Ala Ala Ala Asn Glu Val Tyr Lys Arg Ala  
                          515                      520                      525  
 Lys Ala Leu Asp Gln Ser Asp Asn Asp Met Ser Ala Val Tyr Arg Ala  
                          530                      535                      540  
 Tyr Ile His  
 545

&lt;210&gt; 138

&lt;211&gt; 1097

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

attggttcaa gaagaaaatt tgagcccagg cacccaaaca ccttcaaag ataaagcaag 60  
 tatgttgcaa gaatactcca aatacctcca acaggctttt gaaaaatcca ctaatgcaag 120  
 ttttactctt ggacacgggt tccaatttgt cagtttgtct tcacctctcc acaaccacac 180  
 tttgtttcca gaaaaacaaa tatacactac gtctcctttg gagtgtgggt tcggccaatc 240  
 tgttacctca gtgttgccat cttcattgcc aaagcctcct tttgggatgt tgtttggatc 300  
 tcagccagggt ctttatttgt ctgctttgga tgctacacat cagcagttga caccttccca 360  
 ggagctggat gatctgatag attctcagaa gaacttagag acttcatcag cttccagtc 420  
 ctcactctcag aaattgacta gccagaagga acagaaaaac ttagagtctt caacaggctt 480  
 tcagattcca tctcaggagt tagctagcca gatagatcct cagaaagaca tagagcctag 540  
 aacaacgtat cagattgaga actttgcaca agcgttttgt tctcagttta agtcgggcag 600  
 caggggtgcca atgaccttta tctaactc taatggagaa gtggaccata gagtaaggac 660  
 ttcagtgtca gatttctcag ggtatacaaa tatgatgtct gatgtaagt agccatgtag 720  
 tacaagagta aagacaccca ccagccagag ttacaggtaa ggtcccaaaa gtggccaggc 780  
 tggaggtttt ttaatgtaat tttgttttat tttgagaaca ctgccattgg aatgttttta 840  
 cagcatccta ttaagaataa tgtgatgccc tttcaatgca acttttcata tttagtttat 900  
 tttgttagcg tgatttttagc tctgtttgta ttatgatttt taatcaaaat caatagatta 960  
 aaaatagttt gacattcaaa gtgacaatgt ttagcaatca aatttacatg tatagattgt 1020  
 caggggaatag cccaaatggt ttaaacgcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1080  
 aaaaaaaaaa aaaaaaa 1097

&lt;210&gt; 139

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 139

Met Leu Gln Glu Tyr Ser Lys Tyr Leu Gln Gln Ala Phe Glu Lys Ser  
 1 5 10 15

Thr Asn Ala Ser Phe Thr Leu Gly His Gly Phe Gln Phe Val Ser Leu  
 20 25 30

Ser Ser Pro Leu His Asn His Thr Leu Phe Pro Glu Lys Gln Ile Tyr  
 35 40 45

Thr Thr Ser Pro Leu Glu Cys Gly Phe Gly Gln Ser Val Thr Ser Val  
 50 55 60

Leu Pro Ser Ser Leu Pro Lys Pro Pro Phe Gly Met Leu Phe Gly Ser  
 65 70 75 80

Gln Pro Gly Leu Tyr Leu Ser Ala Leu Asp Ala Thr His Gln Gln Leu  
 85 90 95

Thr Pro Ser Gln Glu Leu Asp Asp Leu Ile Asp Ser Gln Lys Asn Leu  
 100 105 110

Glu Thr Ser Ser Ala Phe Gln Ser Ser Ser Gln Lys Leu Thr Ser Gln  
 115 120 125

Lys Glu Gln Lys Asn Leu Glu Ser Ser Thr Gly Phe Gln Ile Pro Ser  
 130 135 140

Gln Glu Leu Ala Ser Gln Ile Asp Pro Gln Lys Asp Ile Glu Pro Arg  
 145 150 155 160

Thr Thr Tyr Gln Ile Glu Asn Phe Ala Gln Ala Phe Gly Ser Gln Phe  
 165 170 175

Lys Ser Gly Ser Arg Val Pro Met Thr Phe Ile Thr Asn Ser Asn Gly  
 180 185 190

Glu Val Asp His Arg Val Arg Thr Ser Val Ser Asp Phe Ser Gly Tyr  
 195 200 205

Thr Asn Met Met Ser Asp Val Ser Glu Pro Cys Ser Thr Arg Val Lys  
 210 215 220

Thr Pro Thr Ser Gln Ser Tyr Arg  
 225 230

&lt;210&gt; 140

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 140

gtgtcacata ccactcttgt aggtgtcctc aataatcccc ttttccacac aaatacacag 60  
 ggtgtattat ctttctcttt attcaccccc actttgctga actgaagtta attacatagc 120  
 ctttcttcta acctccttag taatgaacct tcacataaag tgtatttaca gcgtctgtcg 180

```

tagccagccc ttcctcctct actttctagc aggggatagc caataactag gaatttaatg 240
acagatTTTT tttttctttg aaataaatgg ccagagtttc tccatttttag aattttgttg 300
tccctcctaa tcatctgctt acctagtcat tactcaatct gcagaaactt cataaaggaa 360
aagtgcgtga ttgtctttac aaataacagt ttgtaggga aatatgacaa acctcaacta 420
tgaggagtgt ccacaataca aaattttgaa aaaacattac atagtataa taccatactt 480
ggttgttagg cttgttgcct ccccatca gaggcattca atgatttatc ttttgaatt 540
gctgtgaact tttttaata agccatttag tgtgaaattg tcatgtatca aatggctatt 600
ggaaatggac tttactcaat ttttaattcca ctgcactcta gccggagtga cagagtaaga 660
ctctgtctca aaaataaata aataaataaa taaataaata aataaataaa taaataaata 720
ataataatac aagttttcat aaggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 775

```

&lt;210&gt; 141

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

```

Met Thr Asn Leu Asn Tyr Gly Ser Cys Pro Gln Tyr Lys Ile Leu Lys
  1             5             10             15

```

```

Lys His Tyr Ile Val Ile Ile Ser Tyr Leu Val Val Arg Leu Val Ala
      20             25             30

```

```

Ser Pro His Gln Arg His Leu Met Ile Tyr Leu Leu
      35             40

```

&lt;210&gt; 142

&lt;211&gt; 2060

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

```

gaaaaagaag acaaagctca ccttcaggcg gaggtgcagc acctgcgaga ggacaacctg 60
aggctacagg aggagtccca gaacgcctcg gacaagctga agaagttcac agaattgggtc 120
ttcaacacca tagacatgag ctagggaagg ctgaggagga caggagaagg gccagacac 180
tccctccagt gagtgtcctg cagcccttat tccctccata gaaagcatcc tcagagcacc 240
ttccctggct tccactctg cccctcttcg gggagtgcac aacacaatag ttgcagatca 300
acaatcatca cctgcctttt gtagaaaaga aaaacaaaaa aagtaataaa aaatttttaa 360
cagtaaaaata aaagtttaac tgctaaaatg tgaatgtcct tatttttttg cacaatatct 420
ttatctgtta tgtatttaag aagaaactgg gccttggacc agggcgcccc ctggcccatc 480
cgccctctatt cccatcagct ttcttatcaa cttcaggtaa cccaagcttt cccttgttat 540
tctaacaaat atcattatcc ctagaaaaag aatgttttta taacttgttt ggggagtaga 600
gagggatatt tccctacctt ctccctaaa atgcctggag agggagtgtc tttgagaaa 660
tgccctaccc ccttgaatga ctctgtcatg agctagtgtc gtctgtacct gtccctccaga 720
gatcagcagg accggagtta aatatttaac agcaagtctg taaaccagag cagctctgac 780
agtgcctgca ggccacaccc ctctcagtc ctgcattgtg aggtcatttc ctgctctctc 840
ctttcccccag gaagatggtc ccacttgtgc tgcaagactc ttttttgttt ggcttaattg 900
agccccacta aattggaatc aatctctctt acagcttccg ggctccaaac attaatgat 960
ttcagaatcc ccccaacta aaaccttatc tgtctgcatt ttgaatgat tttggtcaa 1020
agtatacgtt ttaaagattt ttaaagataa aaatgtggca caactggttt ttttagcttg 1080
ctgaaaaatga ccatactctt aaattaatct ttctctccag agcaagactt caccagtatt 1140
tgtaactagg agaagctaa tgaatgttta attgtgaatt ttaatcattg cttgttagga 1200
ataatgactg tgatactaga atgggctttt gaaacctgca tgtcccagtg tgaatttca 1260
gcacggcatt ttctgcaccc ttctatggcc atccaaagga ttccgctgca gaaattattg 1320
atgtgtctatt tttgtgtct tgtgatgcag gctgctttgg gcccctgggt cactcttcca 1380
aggctgctgt agagcacaga gacatggggc tggccagtgt tgactgacct gaggagaccc 1440
ctttgtttgt tgcttcata actgtcacta aaccgacccc tctgcccctt cagtggcaac 1500
tctgtgtcaa gggaacatcc agcactctag cggcatctga ttggaagttc cctcacccaa 1560
gtaatctcaa ttccttctc tctccatccc tgaaagaaac aggatggatt ttcctctctt 1620

```

```

ctccctgcta cttcactac cagattttta tgctacagtt tcattcttga ttgtgatttc 1680
tccatggaaat tttttttttc tggtagacatt tctatcatgg aaataggaag atttcggagt 1740
gctttgtgaa gatttcaatt gtctgtctct tctctctctt gacttgatg aaggagattg 1800
tacattgcct gatattctct tgtaaatgag aaatattgct aacatccaag cattctgaag 1860
tcttgcttat ccttctgagt ttagttctca ttttgtttta cttttgtttt ggggacttgg 1920
ggcaagctat ttattagagt ttgcaacag agttcttgtt tgaagcctct aaagactacc 1980
tgtaaaaattc aaagaataaaa attcatttta aacgctcttt taaaaaaaaa aaaaaaaaaa 2040
aaaaaaaaaa aaaaaaaaaa 2060

```

&lt;210&gt; 143

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 143

```

Met Thr Val Ile Leu Glu Trp Ala Phe Glu Thr Cys Met Ser Gln Cys
  1             5             10             15

```

```

Glu Ile Ser Ala Arg His Phe Leu His Pro Phe Met Ala Ile Gln Arg
      20             25             30

```

```

Ile Pro Leu Gln Lys Leu Leu Met Cys Tyr Phe Cys Cys Leu Val Met
      35             40             45

```

```

Gln Ala Ala Leu Gly Pro Trp Val Thr Leu Pro Arg Leu Leu
      50             55             60

```

&lt;210&gt; 144

&lt;211&gt; 1160

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 144

```

gattattttc agtaggcaga catctaatacg gaatcttgct cttgttgccc aggctggagt 60
gtaatggcac aatctcggct tactgcaacc tctgctcctt ggattcaagt gattctcctg 120
cctcagcctc ccaagtagct gggattacag cctgaaaaac cactcgcttg cagagcgctg 180
gatcagcaat gcctactagt tcttcattca aacaccggat taaagagcag gaagactaca 240
tccgagattg gactgctcat cgagaagaga tagccaggat cagccaagat cttgctctca 300
ttgctcggga gatcaacgat gtagcaggag agatagattc agtgacttca tcaggcactg 360
cccctagtac cacagtaagc actgctgcca ccacccctgg ctctgccata gacactagag 420
aagagttggt tgatcggtgt tttgatgaaa gcctcaactt ccaaaagatt cctccattag 480
ttcattccaa aacaccagaa ggaaacaacg gtcgatctgg tgatccaaga cctcaagcag 540
cagagcctcc cgatcactta acaattacaa ggcggagaac ctggagcagg gatgaagtca 600
tgaggagataa tctgctgctg tcatccgtct ttcagttctc targaagata agacaatcta 660
tagataagac agctggaaag atcagaatat tatttaaaga caaagatcgg aattgggatg 720
acatagaaag caaattaaga gccgaaagtg aagtccttat tgtgaaaacc tcgagcatgg 780
agatttcttc tatcttacag gaactgaaaa gactagaaaa gcagctacaa gcaatcaatg 840
ctatgattga tccgtatgga actttggagg ctctgaacaa catgggattt cccagtgcata 900
tgttgccatc tccaccgaaa cagaagtcca gccctgtgaa taaccaccac agcccgggtc 960
agacaccaac acttggccaa ccagaagcta gggctcttca tctgctgctt gtttcagccg 1020
cagctgaatt tgagaatgct gaatctgagg ctgatttcag tatacatttc aatagagtca 1080
accctgatgg ggaagaggaa gatgttacag taacataaat gactttctct tgattgttga 1140
aaaaaaaaaa aaaaaaaaaa 1160

```

&lt;210&gt; 145

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens



&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (152)

&lt;400&gt; 145

Met Pro Thr Ser Ser Ser Phe Lys His Arg Ile Lys Glu Gln Glu Asp  
 1 5 10 15

Tyr Ile Arg Asp Trp Thr Ala His Arg Glu Glu Ile Ala Arg Ile Ser  
 20 25 30

Gln Asp Leu Ala Leu Ile Ala Arg Glu Ile Asn Asp Val Ala Gly Glu  
 35 40 45

Ile Asp Ser Val Thr Ser Ser Gly Thr Ala Pro Ser Thr Thr Val Ser  
 50 55 60

Thr Ala Ala Thr Thr Pro Gly Ser Ala Ile Asp Thr Arg Glu Glu Leu  
 65 70 75 80

Val Asp Arg Val Phe Asp Glu Ser Leu Asn Phe Gln Lys Ile Pro Pro  
 85 90 95

Leu Val His Ser Lys Thr Pro Glu Gly Asn Asn Gly Arg Ser Gly Asp  
 100 105 110

Pro Arg Pro Gln Ala Ala Glu Pro Pro Asp His Leu Thr Ile Thr Arg  
 115 120 125

Arg Arg Thr Trp Ser Arg Asp Glu Val Met Gly Asp Asn Leu Leu Leu  
 130 135 140

Ser Ser Val Phe Gln Phe Ser Xaa Lys Ile Arg Gln Ser Ile Asp Lys  
 145 150 155 160

Thr Ala Gly Lys Ile Arg Ile Leu Phe Lys Asp Lys Asp Arg Asn Trp  
 165 170 175

Asp Asp Ile Glu Ser Lys Leu Arg Ala Glu Ser Glu Val Pro Ile Val  
 180 185 190

Lys Thr Ser Ser Met Glu Ile Ser Ser Ile Leu Gln Glu Leu Lys Arg  
 195 200 205

Val Glu Lys Gln Leu Gln Ala Ile Asn Ala Met Ile Asp Pro Asp Gly  
 210 215 220

Thr Leu Glu Ala Leu Asn Asn Met Gly Phe Pro Ser Ala Met Leu Pro  
 225 230 235 240

Ser Pro Pro Lys Gln Lys Ser Ser Pro Val Asn Asn His His Ser Pro  
 245 250 255

Gly Gln Thr Pro Thr Leu Gly Gln Pro Glu Ala Arg Ala Leu His Pro  
 260 265 270

Ala Ala Val Ser Ala Ala Ala Glu Phe Glu Asn Ala Glu Ser Glu Ala  
 275 280 285

Asp Phe Ser Ile His Phe Asn Arg Val Asn Pro Asp Gly Glu Glu Glu

290

295

300

Asp Val Thr Val Thr  
305

&lt;210&gt; 146

&lt;211&gt; 1536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (317)

&lt;400&gt; 146

```

gaagagagaa aatcagcctg tctgctctct ccttggctca acaaggcctc taacagtctt 60
ctgtcctcta ttctgcacac ggcataattg ggaacgagaa acaaaagttt tcccaaata 120
agagaactca cttgtttatt gtggggattt attttctgtc ctcttgcagg gcagaagagg 180
ggcttaattt cccacacat gatgggaagg accgagtggg aagtctttcc gagaagaact 240
tcaagcagg tttaaagaaa tatgacttgc ttgacctcta ctaccatgag ccggtgtctt 300
cagataagg cagcnaaaa cagttccaac tgaaagaaat cgtgcttgag cttgtggccc 360
acgtccttga acataaagct ataggccttg tgatgggtgga tgccaagaaa gaagccaagc 420
ttgccaagaa actgggtttt gatgaagaag gaagcctgta tattcttaag ggtgatcgca 480
caatagagtt tgatggcgag ttgacagctg atgtcttggg ggagtctctc ttggatctaa 540
ttgaagaccc agtggagatc atcagcagca aactggaagt ccaagccttc gaacgcattg 600
aagactacat caaactcatt ggctttttca agagtggaga ctcaataac tacaaggcct 660
ttgaagaagc agctgaacac ttccagcctt acatcaaatt ctttgccacc ttgacaaaag 720
gggttgcaaa gaaattatct ttgaagatga atgaggttga cttctatgag ccatttatgg 780
atgagcccat tgccatcccc aacaaacctt acacagaaga ggagctgggt gagtttgtga 840
aggaacacca aaggtgcctg agatggcatg tgggggctgg gggcctgggg tctggggaat 900
ggagaggagc ctctctgtgc taacatttca gacctgccaa gagcaacaac ctagttagta 960
ccccagcagt acagaactca gtagtatggc ttgtttgatc agtaatgact agcagggatg 1020
ttattacttc tgaatctaag tctgcacctg caagcagagt ttgataaatc cctcagtcag 1080
caaatcccc ccaagccagg gcaagatata aataaaattc tatactagga atgagagcaa 1140
tttagtgaaa gttcccatat accaataacc atgcccagtg ctttagggaa actattttat 1200
ctaacttcca accttaggga gtaattatta ttatcccaat ttacagatc aagggaattg 1260
actcaatagt taagtaactt agccaaggat gaacactcta tgcatagaac ttctgggaga 1320
gaaatgcttg ataccactta gtgtagctcc agcatggatc agcaaacttt ttctgtaaag 1380
aacaaaatgg taaatatttc aggttctgtg ggccagatgg cgtctgtagc aactacttaa 1440
ctgcggctgt ggcatgaaag cagccatgga tcatgtataa acaaatgggt gtggctgtgt 1500
accagtaaaa gtttatttag gaaaaaaaa aaaaaa 1536

```

&lt;210&gt; 147

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (67)

&lt;400&gt; 147

Met Lys Arg Thr His Leu Phe Ile Val Gly Ile Tyr Phe Leu Ser Ser  
1 5 10 15

Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr Tyr Asp Gly Lys Asp  
20 25 30

Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys Gln Val Leu Lys Lys

35                      40                      45  
 Tyr Asp Leu Leu Cys Leu Tyr Tyr His Glu Pro Val Ser Ser Asp Lys  
     50                      55                      60  
 Val Thr Xaa Lys Gln Phe Gln Leu Lys Glu Ile Val Leu Glu Leu Val  
     65                      70                      75                      80  
 Ala His Val Leu Glu His Lys Ala Ile Gly Phe Val Met Val Asp Ala  
                     85                      90                      95  
 Lys Lys Glu Ala Lys Leu Ala Lys Lys Leu Gly Phe Asp Glu Glu Gly  
                     100                      105                      110  
 Ser Leu Tyr Ile Leu Lys Gly Asp Arg Thr Ile Glu Phe Asp Gly Glu  
                     115                      120                      125  
 Phe Ala Ala Asp Val Leu Val Glu Phe Leu Leu Asp Leu Ile Glu Asp  
                     130                      135                      140  
 Pro Val Glu Ile Ile Ser Ser Lys Leu Glu Val Gln Ala Phe Glu Arg  
                     145                      150                      155                      160  
 Ile Glu Asp Tyr Ile Lys Leu Ile Gly Phe Phe Lys Ser Glu Asp Ser  
                     165                      170                      175  
 Glu Tyr Tyr Lys Ala Phe Glu Glu Ala Ala Glu His Phe Gln Pro Tyr  
                     180                      185                      190  
 Ile Lys Phe Phe Ala Thr Phe Asp Lys Gly Val Ala Lys Lys Leu Ser  
                     195                      200                      205  
 Leu Lys Met Asn Glu Val Asp Phe Tyr Glu Pro Phe Met Asp Glu Pro  
                     210                      215                      220  
 Ile Ala Ile Pro Asn Lys Pro Tyr Thr Glu Glu Glu Leu Val Glu Phe  
                     225                      230                      235                      240  
 Val Lys Glu His Gln Arg Cys Leu Arg Trp His Val Gly Ala Gly Gly  
                     245                      250                      255  
 Leu Gly Ser Gly Glu Trp Arg Gly Ala Ser Leu Cys  
                     260                      265

&lt;210&gt; 148

&lt;211&gt; 1009

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

gaattcggcc ttcatgcgcc tgcaggaaag aatctgacat catcacactg tgttttcctt 60  
 aacttgacag gaagtcaact tcaagcagat tgacttgaaa cgggatctca ttttaggaagc 120  
 ataagtgtcc aatcaaaaac tgtgtatctt tttaaatttg gaaaatactc aagttccagt 180  
 tgcttatcat tctccttcac tttctgaaaa cctggcaatc ccatgtggac ttctggtaga 240  
 atgagcaatg caaagaactg gcttggactt ggcatgtcct tgtacttctg ggggctgatg 300  
 gaccttacga ccaccgttct ctcggacacc ccaacaccac aaggtgaatt agaagcactc 360  
 ctgtcagaca agccacagtc acatcagcgg accaagarga gctgggtttg gaaccagttt 420  
 ttcgtttctg aagagtacac tgggaccgac cctttgtatg tcggcaaggt aagaaatgcc 480  
 aagtagaat gacccgggta gtggatattg aaattgaata tgaattgagt atcaaagttg 540

```

acctagcctt tatytgagac ctgagaaaaa ctagaacaag tggtagctta cttgacacct 600
agctaaaaatg taacttctgc ttgtcagag accagtctga aaggaaagat ttatttcctt 660
gtccatgtct ctggtatgaa tgggaaaaag tgggaattgg gatttgaggg aaaaggctca 720
gacctgcaa gagctattca agtcctaaaa gaggcagcag cagctgtctg ggaatgacag 780
aatgggggag agggaaactt ggaaatacaa gaagagtaca gagttttttg ctttgtgttt 840
ttatgggggt tttttcagag cattttccaga ggtattgcct gaggtgcaaa tttaatgaaa 900
aaaataaaaa taaaacattt ttcatttcag aagatcttag catgtgcttt aggatagtgtg 960
gagacaataa atatatttat aaatgttaaa aaaaaaaaaa aaaaaaaaaa 1009

```

&lt;210&gt; 149

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (59)

&lt;400&gt; 149

```

Met Trp Thr Ser Gly Arg Met Ser Asn Ala Lys Asn Trp Leu Gly Leu
  1             5             10             15

```

```

Gly Met Ser Leu Tyr Phe Trp Gly Leu Met Asp Leu Thr Thr Thr Val
          20             25             30

```

```

Leu Ser Asp Thr Pro Thr Pro Gln Gly Glu Leu Glu Ala Leu Leu Ser
      35             40             45

```

```

Asp Lys Pro Gln Ser His Gln Arg Thr Lys Xaa Ser Trp Val Trp Asn
      50             55             60

```

```

Gln Phe Phe Val Leu Glu Glu Tyr Thr Gly Thr Asp Pro Leu Tyr Val
      65             70             75             80

```

```

Gly Lys Val Arg Asn Ala Lys
          85

```

&lt;210&gt; 150

&lt;211&gt; 2546

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 150

```

aaaagaaacc aaggaaattt gtatgataag gcaggtaaag tgaggaaaca tgcaactgaa 60
caggaaaaaa ctgaagaggg attaggccct aatataaaaa gcattgtcac catgttgatg 120
ctgatgctat tgatgatgtt tgctgtccac tgtacctggg tcacaagcaa tgccactact 180
agtccaagtg tagtcctggc ctcatacaat catgatggca ccaggaatat cttagatgat 240
tttagagaag cttacttttg gctaaggcaa aatacagatg aacatgcacg agtaatgtct 300
tgggtgggatt atggctatca gatagctgga atggctaata gaactacggt ggtggataat 360
aacacctgga ataacagcca catagcactg gtgggaaaag ctatgtcttc taatgaaaca 420
gcagcctata aaatcatgag gactctagat gtagattatg ttttggttat ttttgagggg 480
gttattggct attctggtga tgatatcaac aaatttctct ggatggttag gatagctgaa 540
ggagaacatc ccaaagacat tcgggaaagt gactatttta cccacagggg agaattccgt 600
gtagacaaag caggatcccc tactttgttg aattgcctta tgtataaaat gtcatactac 660
agatttgag aaatgcagct ggattttcgt acacccccag gttttgaccg aacacgtaat 720
gctgagattg gaaataagga cattaaattc aaacatttgg aagaagcctt tacatcagaa 780
cactggcttg ttaggatata taaagtaaaa gcacctgata acagggagac attagatcac 840
aaacctcgag tcaccaacat tttcccaaaa cagaagtatt tgtcaaagaa gactaccaa 900
aggaagcgtg gctacattaa aaataagctg gtttttaaga aaggcaagaa aatatctaag 960

```

```

aagactgttt aaatgcactg ttctgggtcc taacttgaag cagttgtcct tgtgagaacc 1020
ggctctttgcc ttttagctcat gtcgtgtttc acagcaaaga gggtagacaga ccatcactgg 1080
tccagggttaa tgtacaaaat tttctggcaa tgcctgatta aaaaaataaa attggcttgt 1140
tgagaacagc tgttttcgat ttctaattgt aagcaagaca gagcactgct gtaaatgtct 1200
agcagcagat ttttttttta ttggtacata ttatccttca aatctgagaa tttggactaa 1260
ctgcacaaaa gaacctctta atttgggtccc tggcacatgc atacttgtca atgtttttat 1320
tctcttacaa gacctgcatt ttatttgaat taccgaata gcaatatgta aaatacaagt 1380
gacaaaatgt gatgagagct tcttgaaccg gtaaaactagt acaggtctga gaaagacata 1440
ttagaagaat cattatactt ccttgaatta tttttatttt catgtttctc taatgcaaag 1500
aatgtttcat caaatgtata ttttctgttg cttactgttt gctctgagaa gaagctgctg 1560
tttcaaagat ggacctctga gtagctaatt gattcaagta gtttttttat gttgacacat 1620
tattactgct gttagcagtc gttttcacca ggtacttaca gagcagattt catacatcat 1680
tcattcaagg gctaaattta ttttttttgg aaatcatggc aactacacag gatgttgctt 1740
accaggacgg agtttttggt tcttagtact gaagttagca ctatgtttac atgcaaaaaga 1800
ttaaggaaaa aacctttaa gtggacaggt atccaaagtt cattttctgt gactcatcaa 1860
agtgaacaaa gacttgtaac aactttgcct ggactttttt cattttacaa cagttcatcc 1920
attcacaatg attttgttct ctgtccata ttttttaac ccttaagcat ttgatgaaac 1980
actctttagt gctatatgca ttttcttact tttgttaaaa atgtgacaat tgtcaaaaaa 2040
tgcactaaaa tgtaaatgga gattgaacaa gttcactttc cagcttatag gcaactttat 2100
acagacttga acattttctc cagtgttcta gtaaaagtga aagagaaagg gtttttcctg 2160
ccacaggata taactttttt ttatataaca agcataacac accactgctt ttggtggaaa 2220
agtgcagaat agtatgtacc ttttatgaag aaaaatgtaa ttacaatat tcagtgagaa 2280
tgttactgct gattttcttt tccaagggtt agaataattt ttgatttata gaattcattt 2340
ttgaccaga tgaagggtcc ttacagaaac aataaaatgg ctgaacattt tcacaaatag 2400
agtgtaacga agtctggatt tctgatacct tgtcatttgg gggattttat tttactttgt 2460
tgctttaaaa ttcaatgcag agaatgtgtt gactgtaggg gaaataaagt taattcaaat 2520
ttgaaaaaaa aaaaaaaaaa aaaaaa
2546

```

&lt;210&gt; 151

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 151

```

Met Leu Met Leu Met Leu Leu Met Met Phe Ala Val His Cys Thr Trp
  1              5              10              15

Val Thr Ser Asn Ala Tyr Ser Ser Pro Ser Val Val Leu Ala Ser Tyr
          20              25              30

Asn His Asp Gly Thr Arg Asn Ile Leu Asp Asp Phe Arg Glu Ala Tyr
          35              40              45

Phe Trp Leu Arg Gln Asn Thr Asp Glu His Ala Arg Val Met Ser Trp
          50              55              60

Trp Asp Tyr Gly Tyr Gln Ile Ala Gly Met Ala Asn Arg Thr Thr Leu
          65              70              75              80

Val Asp Asn Asn Thr Trp Asn Asn Ser His Ile Ala Leu Val Gly Lys
          85              90              95

Ala Met Ser Ser Asn Glu Thr Ala Ala Tyr Lys Ile Met Arg Thr Leu
          100             105             110

Asp Val Asp Tyr Val Leu Val Ile Phe Gly Gly Val Ile Gly Tyr Ser
          115             120             125

Gly Asp Asp Ile Asn Lys Phe Leu Trp Met Val Arg Ile Ala Glu Gly
          130             135             140

```

Glu His Pro Lys Asp Ile Arg Glu Ser Asp Tyr Phe Thr Pro Gln Gly  
 145 150 155 160  
 Glu Phe Arg Val Asp Lys Ala Gly Ser Pro Thr Leu Leu Asn Cys Leu  
 165 170 175  
 Met Tyr Lys Met Ser Tyr Tyr Arg Phe Gly Glu Met Gln Leu Asp Phe  
 180 185 190  
 Arg Thr Pro Pro Gly Phe Asp Arg Thr Arg Asn Ala Glu Ile Gly Asn  
 195 200 205  
 Lys Asp Ile Lys Phe Lys His Leu Glu Glu Ala Phe Thr Ser Glu His  
 210 215 220  
 Trp Leu Val Arg Ile Tyr Lys Val Lys Ala Pro Asp Asn Arg Glu Thr  
 225 230 235 240  
 Leu Asp His Lys Pro Arg Val Thr Asn Ile Phe Pro Lys Gln Lys Tyr  
 245 250 255  
 Leu Ser Lys Lys Thr Thr Lys Arg Lys Arg Gly Tyr Ile Lys Asn Lys  
 260 265 270  
 Leu Val Phe Lys Lys Gly Lys Lys Ile Ser Lys Lys Thr Val  
 275 280 285

&lt;210&gt; 152

&lt;211&gt; 4061

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

aagcaattga agaaattgca gcaggatgtg atggaaatga aaaaaacaaa ggttcgccta 60  
 atgaaacaaa tgaaagaaga acaagagaaa gccagactga ctgagtctag aagaaacaga 120  
 gagattgtct agttgaaaaa ggatcaacgt aaaagagatc atcmacttag acttctggaa 180  
 gcccaaaaaa gaaaccaaga agtggttcta cgtcgcaaaa ctgaagaggt tacggctctt 240  
 cgtcggcaag taagacccat gtcagataaa gtggctggga aagttactcg gaagctgagt 300  
 tcatctgatg cacctgctca ggacacaggt tccagtgcag ctgctgtcga aacagatgca 360  
 tcaaggacag gagcccagca gaaaatgaga attcctgtgg cgagagtcca ggccttacca 420  
 acgccggcaa caaatggaaa caggaaaaaa tatcagagga aaggattgac tggccgagtg 480  
 tttatttcca agacagctcg catgaagtgg cagctccttg agcgcagggc cacagacatc 540  
 atcatgcaga agatgaccat ttccaacatg gaggcagata tgaatagact cctcaagcaa 600  
 cgggagggaac tcacaaaaag acgagagaaa ctttcaaaaa gaaggagaaa gatagtcaag 660  
 gagaatggag agggagataa aaatgtggct aatatcaatg aagagatgga gtcactgact 720  
 gctaatatcg attacatcaa tgacagtatt tctgattgtc aggccaacat aatgcagatg 780  
 gaagaagcaa aggaagaagg tgagacattg gatgttactg cagtcattaa tgcctgcacc 840  
 cttacagaag cccgatacct gctagatcac ttccctgtcaa tgggcatcaa taagggtctt 900  
 caggctgccc agaaagaggc tcaaattaaa gtactggaag gtcgactcaa acaaacagaa 960  
 ataaccagtg ctacccaaaa ccagctctta ttccatattg tgaaagagaa ggcagaatta 1020  
 aatcctgagc tagatgcttt actaggccat gctttacaag atctagatag cgtaccatta 1080  
 gaaaaatgtag aggatagtac tgatgaggat gctcctttaa acagcccagg atcagaagga 1140  
 agcacgctgt cttcagatct catgaagctt tgtggtgaag tgaaacctaa gaacaaggcc 1200  
 cgaaggagaa ccaccactca gatggaattg ctgtatgcag atagcagtga actagcttca 1260  
 gacactagta caggagatgc ctcccttgct ggccctctca cactgttgc agaagggcaa 1320  
 gagattggaa tgaatacaga gacaagtggt acttctgcta gggaaaaaga gctctctccc 1380  
 ccacctggct tactttctaa gataggcagc atttccaggc agtcatctct atcagaaaaa 1440  
 aaaattccag agccttctec tgtaacaagg agaaaggcat atgagaaagc agaaaaatca 1500

```

aaggccaagg aacaaaagca ctccagattct ggaacttcag aggctagtct ttcacctcct 1560
tcttccccac caagccggcc ccgtaaatgaa ctgaaatgtt ttaatcgtct tactgtttct 1620
cagggaaaca catcagttca gcaggataag tctgatgaaa gtgactcctc tctctcggag 1680
gtacacagca gatcctccag aaggggcata atcaacccat ttcctgcttc aaaaggaatc 1740
agagcttttc cacttcagtg tattcacata gctgaagggc atacaaaagc tgtgctctgt 1800
gtggattcta ctgatgatct cctcttcact ggatcaaaaag atcgtacttg taaagtatgg 1860
aatctgggtga ctgggcagga aataatgtca ctgggggggc atcccaacaa tgtcgtgtct 1920
gtaaaataact gtaattatac cagtttggtc ttcactgtat caacatctta tattaaggtg 1980
tgggatatca gagattcagc aaagtgcatt cgaacactaa cgtcttcagg tcaagttact 2040
cttgagagatg cttgttctgc aagtaccagt cgaacagtag ctattccttc tggagagaac 2100
cagatcaatc aaattgccct aaacccaact ggcaccttcc tctatgctgc ttctggaaat 2160
gctgtcagga tgtgggatct taaaagggtt cagtctacag gaaagttaac aggacaccta 2220
ggccctgtta tgtgccttac tgtggatcag atttccagtg gacaagatct aatcatcact 2280
ggctccaagg atcattacat caaaatgttt gatgttacag aaggagctct tgggactgtg 2340
agtccacccc acaattttga accccctcat tatgatggca tagaagcact aaccattcaa 2400
ggggataacc tatttagtgg gtctagagat aatggaatca agaaatggga cttactcaa 2460
aaagaccttc ttcagcaagt tccaaatgca cataaggatt gggctctgtc cctgggagtg 2520
gtgccagacc acccagtttt gctcagtgcc tgcagagggg gcattttgaa agtctggaac 2580
atggatactt ttatgccagt gggagagatg aagggtcatg atagtcctat caatgccata 2640
tgtgttaatt ccaccacat ttttactgca gctgatgatc gaactgtgag aatttggag 2700
gctcgcaatt tgcagatggg tcagatctct gacacaggag atctggggga agatattgcc 2760
agtaattaaa catgaatgaa gatagggtgt aaactgaatg ctgtgataat actctgtatt 2820
ctttatggaa aatgttgctc tgtacttact aggcaaaacg tatgaatcgg attactgga 2880
aaatatatct gaattcaact gctgactata aatgggtatc taataaaatt gtgtactatc 2940
ctgtgtgctt agttttaaga tcaaccaata gatatatatc ctacaattga tatattgctt 3000
tattcacact ttatttggg ctgaattttt gtgcctatct ataaaacaca ctttcaaatt 3060
atttgaatta ccaagacgtc tgcctttgtg acagtcagaa aacacacctg gaatacgtg 3120
cagccacca ttaactcatt catgtagttt attcaagtga tttatgtatt taaactaaat 3180
attgaaaatg ttagtcaaat tgtggtttgc ttgtcaggta tttatatcag tctgtagtgg 3240
attcccaaat tcaaaagctc ttttaaatga atggacaaaa ataagatatg agaattatt 3300
tgatgaattt tcataagggt gaattgatct taatctacta acagagaagg gtagacagtt 3360
tgtgttaaat ttgggcattt acctgtattg accaaagctt tgcagctcta ctatattctg 3420
tgctcaggac taaaatgctg ttaatttttt tttttttttt tccagtgtg tgcatatatt 3480
ctgtgatggg aaacattgtt gatgtcctaa cagaaatata ttttgatcta ttttcctatg 3540
gagttgtttc tattatgacc atttaatttt gtttttattt aatagtagta tttccttccc 3600
ttttatctaa ttttttatat gctgctaaat atattttaaa cactactatg ttgcgaacct 3660
tggtagctat gatgagagct attatcatct gtggtgggaa aagctatgta aataggtaga 3720
ttgtatagag agactatctt gtgttgtgct tgtatgaact tttaaaagtt gttgactgga 3780
ttttgcaaaa ggatgtataa ttttctgctc tgcctcagaat attaatgtgt aaattctgca 3840
agtttaattt ttatgtatag ggtataacat ttgaaaatat tgtcttatgt gattttttcc 3900
cctgaaaaata ttgtcttcta aatgaaaact tagctagggc ttaataaaac atgttgctat 3960
gaaatkraaa aaaaaaaaaa aaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4020
aaraaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 4061

```

&lt;210&gt; 153

&lt;211&gt; 910

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (43)

&lt;400&gt; 153

Met Lys Lys Thr Lys Val Arg Leu Met Lys Gln Met Lys Glu Glu Gln  
1 5 10 15

Glu Lys Ala Arg Leu Thr Glu Ser Arg Arg Asn Arg Glu Ile Ala Gln  
20 25 30

Leu Lys Lys Asp Gln Arg Lys Arg Asp His Xaa Leu Arg Leu Leu Glu  
 35 40 45  
 Ala Gln Lys Arg Asn Gln Glu Val Val Leu Arg Arg Lys Thr Glu Glu  
 50 55 60  
 Val Thr Ala Leu Arg Arg Gln Val Arg Pro Met Ser Asp Lys Val Ala  
 65 70 75 80  
 Gly Lys Val Thr Arg Lys Leu Ser Ser Ser Asp Ala Pro Ala Gln Asp  
 85 90 95  
 Thr Gly Ser Ser Ala Ala Ala Val Glu Thr Asp Ala Ser Arg Thr Gly  
 100 105 110  
 Ala Gln Gln Lys Met Arg Ile Pro Val Ala Arg Val Gln Ala Leu Pro  
 115 120 125  
 Thr Pro Ala Thr Asn Gly Asn Arg Lys Lys Tyr Gln Arg Lys Gly Leu  
 130 135 140  
 Thr Gly Arg Val Phe Ile Ser Lys Thr Ala Arg Met Lys Trp Gln Leu  
 145 150 155 160  
 Leu Glu Arg Arg Val Thr Asp Ile Ile Met Gln Lys Met Thr Ile Ser  
 165 170 175  
 Asn Met Glu Ala Asp Met Asn Arg Leu Leu Lys Gln Arg Glu Glu Leu  
 180 185 190  
 Thr Lys Arg Arg Glu Lys Leu Ser Lys Arg Arg Glu Lys Ile Val Lys  
 195 200 205  
 Glu Asn Gly Glu Gly Asp Lys Asn Val Ala Asn Ile Asn Glu Glu Met  
 210 215 220  
 Glu Ser Leu Thr Ala Asn Ile Asp Tyr Ile Asn Asp Ser Ile Ser Asp  
 225 230 235 240  
 Cys Gln Ala Asn Ile Met Gln Met Glu Glu Ala Lys Glu Glu Gly Glu  
 245 250 255  
 Thr Leu Asp Val Thr Ala Val Ile Asn Ala Cys Thr Leu Thr Glu Ala  
 260 265 270  
 Arg Tyr Leu Leu Asp His Phe Leu Ser Met Gly Ile Asn Lys Gly Leu  
 275 280 285  
 Gln Ala Ala Gln Lys Glu Ala Gln Ile Lys Val Leu Glu Gly Arg Leu  
 290 295 300  
 Lys Gln Thr Glu Ile Thr Ser Ala Thr Gln Asn Gln Leu Leu Phe His  
 305 310 315 320  
 Met Leu Lys Glu Lys Ala Glu Leu Asn Pro Glu Leu Asp Ala Leu Leu  
 325 330 335  
 Gly His Ala Leu Gln Asp Leu Asp Ser Val Pro Leu Glu Asn Val Glu  
 340 345 350



Asp Ser Thr Asp Glu Asp Ala Pro Leu Asn Ser Pro Gly Ser Glu Gly  
 355 360 365  
 Ser Thr Leu Ser Ser Asp Leu Met Lys Leu Cys Gly Glu Val Lys Pro  
 370 375 380  
 Lys Asn Lys Ala Arg Arg Arg Thr Thr Thr Gln Met Glu Leu Leu Tyr  
 385 390 395 400  
 Ala Asp Ser Ser Glu Leu Ala Ser Asp Thr Ser Thr Gly Asp Ala Ser  
 405 410 415  
 Leu Pro Gly Pro Leu Thr Pro Val Ala Glu Gly Gln Glu Ile Gly Met  
 420 425 430  
 Asn Thr Glu Thr Ser Gly Thr Ser Ala Arg Glu Lys Glu Leu Ser Pro  
 435 440 445  
 Pro Pro Gly Leu Pro Ser Lys Ile Gly Ser Ile Ser Arg Gln Ser Ser  
 450 455 460  
 Leu Ser Glu Lys Lys Ile Pro Glu Pro Ser Pro Val Thr Arg Arg Lys  
 465 470 475 480  
 Ala Tyr Glu Lys Ala Glu Lys Ser Lys Ala Lys Glu Gln Lys His Ser  
 485 490 495  
 Asp Ser Gly Thr Ser Glu Ala Ser Leu Ser Pro Pro Ser Ser Pro Pro  
 500 505 510  
 Ser Arg Pro Arg Asn Glu Leu Asn Val Phe Asn Arg Leu Thr Val Ser  
 515 520 525  
 Gln Gly Asn Thr Ser Val Gln Gln Asp Lys Ser Asp Glu Ser Asp Ser  
 530 535 540  
 Ser Leu Ser Glu Val His Ser Arg Ser Ser Arg Arg Gly Ile Ile Asn  
 545 550 555 560  
 Pro Phe Pro Ala Ser Lys Gly Ile Arg Ala Phe Pro Leu Gln Cys Ile  
 565 570 575  
 His Ile Ala Glu Gly His Thr Lys Ala Val Leu Cys Val Asp Ser Thr  
 580 585 590  
 Asp Asp Leu Leu Phe Thr Gly Ser Lys Asp Arg Thr Cys Lys Val Trp  
 595 600 605  
 Asn Leu Val Thr Gly Gln Glu Ile Met Ser Leu Gly Gly His Pro Asn  
 610 615 620  
 Asn Val Val Ser Val Lys Tyr Cys Asn Tyr Thr Ser Leu Val Phe Thr  
 625 630 635 640  
 Val Ser Thr Ser Tyr Ile Lys Val Trp Asp Ile Arg Asp Ser Ala Lys  
 645 650 655  
 Cys Ile Arg Thr Leu Thr Ser Ser Gly Gln Val Thr Leu Gly Asp Ala  
 660 665 670

Cys Ser Ala Ser Thr Ser Arg Thr Val Ala Ile Pro Ser Gly Glu Asn  
 675 680 685  
 Gln Ile Asn Gln Ile Ala Leu Asn Pro Thr Gly Thr Phe Leu Tyr Ala  
 690 695 700  
 Ala Ser Gly Asn Ala Val Arg Met Trp Asp Leu Lys Arg Phe Gln Ser  
 705 710 715 720  
 Thr Gly Lys Leu Thr Gly His Leu Gly Pro Val Met Cys Leu Thr Val  
 725 730 735  
 Asp Gln Ile Ser Ser Gly Gln Asp Leu Ile Ile Thr Gly Ser Lys Asp  
 740 745 750  
 His Tyr Ile Lys Met Phe Asp Val Thr Glu Gly Ala Leu Gly Thr Val  
 755 760 765  
 Ser Pro Thr His Asn Phe Glu Pro Pro His Tyr Asp Gly Ile Glu Ala  
 770 775 780  
 Leu Thr Ile Gln Gly Asp Asn Leu Phe Ser Gly Ser Arg Asp Asn Gly  
 785 790 795 800  
 Ile Lys Lys Trp Asp Leu Thr Gln Lys Asp Leu Leu Gln Gln Val Pro  
 805 810 815  
 Asn Ala His Lys Asp Trp Val Cys Ala Leu Gly Val Val Pro Asp His  
 820 825 830  
 Pro Val Leu Leu Ser Gly Cys Arg Gly Gly Ile Leu Lys Val Trp Asn  
 835 840 845  
 Met Asp Thr Phe Met Pro Val Gly Glu Met Lys Gly His Asp Ser Pro  
 850 855 860  
 Ile Asn Ala Ile Cys Val Asn Ser Thr His Ile Phe Thr Ala Ala Asp  
 865 870 875 880  
 Asp Arg Thr Val Arg Ile Trp Lys Ala Arg Asn Leu Gln Asp Gly Gln  
 885 890 895  
 Ile Ser Asp Thr Gly Asp Leu Gly Glu Asp Ile Ala Ser Asn  
 900 905 910

&lt;210&gt; 154

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 154

aatcgcacct gtccaacttg caatgacttc catggacttg tgcagaaaat catggagcta 60  
 caggatattt tagccaaaac atcagccaag ctgtctcgag ctgaacagcg aatgaataga 120  
 ttggatcagt gctatttgta aaggacttgc accatgaagg gaaccaccta ccgagaattt 180  
 gagtccctgga tagacggctg taagaactgc acatgcctga atggaaccat ccagtgtgaa 240  
 actctaattc gcccaaatcc tgactgcccc cttaagtcgg ctcttgcgta tgtggatggc 300  
 aaatgctgta aggaatgcaa atcgatattc caatttcaag gacgaacctt ctttgaagga 360  
 gaaagaaata ca 372

<210> 155  
 <211> 761  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (108)

<220>  
 <221> unsure  
 <222> (191)

<220>  
 <221> unsure  
 <222> (268)

<220>  
 <221> unsure  
 <222> (299)

<400> 155  
 ttctggagta tgtgttctct atgagtgcaa ggaccagacc atgaaatttg ttgagagttc 60  
 aggctgtcca gctttggatt gtccagagtc tcatcagata accttgtntc acagctgttg 120  
 caaagtgttg aaagggttatg atttttgttt tgaaaggcat aactgcatgg agaattccat 180  
 ctgcagaaat ntgaatgaca gggtgtgttg tagctgtcga gatgggttta gggtttttcg 240  
 agaggataat gcctactgtg aagacatnga tgagtgtgct gaagggcgcc attactgtng 300  
 tgaaaataca atgtgtgtca acaccccggt ttcttttatg tgcattctgca aaactggata 360  
 catcagaatt gatgattatt catgtacaga acatgatgag tgtatcaca atcagcacag 420  
 ctgtgatgaa aatgctttat gcttcaacac tgttggagga cacaactgtg tttgcaagcc 480  
 gggctataca gggatggaa cgacatgcaa agcattttgc aaagatggct gtaggaatgg 540  
 aggagcctgt attgccgcta atgtgtgtgc ctgcccacaa ggcttcactg gacccagctg 600  
 tgaaacggac attgatgaat gctctgatgg ttttgttcaa tgtgacagtc gtgctaattg 660  
 cattaacctg cctggatggt accactgtga gtgcagagat ggctaccatg acaatgggat 720  
 gttttcacca agtggagaat cgtgtgaaga tattgatgag t 761

<210> 156  
 <211> 240  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (23)

<220>  
 <221> UNSURE  
 <222> (51)

<220>  
 <221> UNSURE  
 <222> (76)

<220>  
 <221> UNSURE  
 <222> (87)

<400> 156  
 Met Lys Phe Val Glu Ser Ser Gly Cys Pro Ala Leu Asp Cys Pro Glu  
 1 5 10 15

Ser His Gln Ile Thr Leu Xaa His Ser Cys Cys Lys Val Cys Lys Gly  
 20 25 30  
 Tyr Asp Phe Cys Phe Glu Arg His Asn Cys Met Glu Asn Ser Ile Cys  
 35 40 45  
 Arg Asn Xaa Asn Asp Arg Ala Val Cys Ser Cys Arg Asp Gly Phe Arg  
 50 55 60  
 Val Phe Arg Glu Asp Asn Ala Tyr Cys Glu Asp Xaa Asp Glu Cys Ala  
 65 70 75 80  
 Glu Gly Arg His Tyr Cys Xaa Glu Asn Thr Met Cys Val Asn Thr Pro  
 85 90 95  
 Gly Ser Phe Met Cys Ile Cys Lys Thr Gly Tyr Ile Arg Ile Asp Asp  
 100 105 110  
 Tyr Ser Cys Thr Glu His Asp Glu Cys Ile Thr Asn Gln His Ser Cys  
 115 120 125  
 Asp Glu Asn Ala Leu Cys Phe Asn Thr Val Gly Gly His Asn Cys Val  
 130 135 140  
 Cys Lys Pro Gly Tyr Thr Gly Asn Gly Thr Thr Cys Lys Ala Phe Cys  
 145 150 155 160  
 Lys Asp Gly Cys Arg Asn Gly Gly Ala Cys Ile Ala Ala Asn Val Cys  
 165 170 175  
 Ala Cys Pro Gln Gly Phe Thr Gly Pro Ser Cys Glu Thr Asp Ile Asp  
 180 185 190  
 Glu Cys Ser Asp Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile  
 195 200 205  
 Asn Leu Pro Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp  
 210 215 220  
 Asn Gly Met Phe Ser Pro Ser Gly Glu Ser Cys Glu Asp Ile Asp Glu  
 225 230 235 240

<210> 157  
 <211> 342  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 gcagaaaaatt ttcctctaga tcagaatctt caagaatcag ttaggttcct cactgcaaga 60  
 aataaaatgt caggcagtga atgaattata ttttaagaag taaagcaaag aagctataac 120  
 atgttatgta cagtacactc tgaaaagaaa tctgaaacaa gttattgtaa tgataaaaat 180  
 aatgcacagg catggttact taatattttc taacaggaaa agtcatccct atttccttgt 240  
 ttactgcac ttaatatatt ttggttgaat ttgttcagta taagttcgtt ccttctgcaa 300  
 aattaataaa atatttttct taccttaaaa aaaaaaaaaa aa 342

<210> 158  
 <211> 1445  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 158

```

gtgcgcacatgg ggaacgtata gcaattcggt tgcgtgcctt cctctccttc gaagatgaca 60
aggcctacca tcgtttcttc ctgcctttgg gccgtcaggc agttgggttg gacccgctcc 120
aaccctcggt tcttcctgca atacagtggg tacaatttgt catggctact ctgagataag 180
accacttttt tatctgagct tctgtgacct gctcctggga ctttgcctgg tcacggagac 240
acttctctat ggagcttcag tagcaaataa ggacatcatc tgctataacc tacaagcagt 300
tggacagata ttctacattt cctcatttct ctacaccgtc aattacatct ggtattttga 360
cacagagctg aggatgaaac acacccaaag tggacagagc acatctccac tggatgata 420
ttatacttgt cgattttgtc aaatggcctt tgttttctca agcctgatac ctctgctatt 480
gatgacacct gtattctgtc tgggaaatac tagtgaatgt ttccaaaact tcagtcagag 540
ccacaattgt atcttgatgc actcaccacc atcagccatg gctgaacttc caccttctgc 600
caacacatct gctctgtagc cactttatct ttatgggtat gccattttcc tgggcagctt 660
tgtaactcagc ctctctacca ttatgggtct acttatccga gcccagacat tgtataagaa 720
gtttgtgaag tcaactggct ttctggggag tgaacagtgg gcagtgatcc acattgtgga 780
ccaacgggtg cgcttctacc cagtggcctt cttttgctgc tggggccag ctgtcattct 840
aatgatcata aagctgacta agccacagga caccaagctt cacatggccc tttatgttct 900
ccaggtctta acggaacat ctccaggtct actcaactgt ggagtatatg gctggacgca 960
gcacaaattc caccaactaa agcaggaggg tcggcgtgat gcagataccc agacaccatt 1020
attatgctca cagaagagat tctatagcag gggcttaaat tcaactggaat ccaccctgac 1080
tttctctgcc agtacttcta ccattttttg aaactacaat actggaacat ccaggaactg 1140
gagtatttct acgctaattg attggaaga atgttgggaa aggacatctt aaatcttttc 1200
taactatgcc ctaaactgca gaactcaaag gaaatatagt gccattgtta gtagtcattc 1260
tagatgaatt gggagtatct ctccagttat tccagattc actagtatc cttaaagtct 1320
ctattcaggg agaggaagac actttccatc tcagagatag actcgtgtta ctttgatgga 1380
tattggattt gtctaagtct cttctagaaa aaataaattc tagattatta aaaaaaaaaa 1440
aaaaa

```

1445

&lt;210&gt; 159

&lt;211&gt; 245

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

```

Met Lys His Thr Gln Ser Gly Gln Ser Thr Ser Pro Leu Val Ile Asp
  1              5              10              15

Tyr Thr Cys Arg Phe Cys Gln Met Ala Phe Val Phe Ser Ser Leu Ile
      20              25              30

Pro Leu Leu Leu Met Thr Pro Val Phe Cys Leu Gly Asn Thr Ser Glu
      35              40              45

Cys Phe Gln Asn Phe Ser Gln Ser His Asn Cys Ile Leu Met His Ser
      50              55              60

Pro Pro Ser Ala Met Ala Glu Leu Pro Pro Ser Ala Asn Thr Ser Val
      65              70              75              80

Cys Ser Thr Leu Tyr Phe Tyr Gly Ile Ala Ile Phe Leu Gly Ser Phe
      85              90              95

Val Leu Ser Leu Leu Thr Ile Met Val Leu Leu Ile Arg Ala Gln Thr
      100              105              110

Leu Tyr Lys Lys Phe Val Lys Ser Thr Gly Phe Leu Gly Ser Glu Gln
      115              120              125

Trp Ala Val Ile His Ile Val Asp Gln Arg Val Arg Phe Tyr Pro Val

```

130                      135                      140  
 Ala Phe Phe Cys Cys Trp Gly Pro Ala Val Ile Leu Met Ile Ile Lys  
 145                      150                      155                      160  
 Leu Thr Lys Pro Gln Asp Thr Lys Leu His Met Ala Leu Tyr Val Leu  
                     165                      170                      175  
 Gln Ala Leu Thr Ala Thr Ser Gln Gly Leu Leu Asn Cys Gly Val Tyr  
                     180                      185                      190  
 Gly Trp Thr Gln His Lys Phe His Gln Leu Lys Gln Glu Ala Arg Arg  
                     195                      200                      205  
 Asp Ala Asp Thr Gln Thr Pro Leu Leu Cys Ser Gln Lys Arg Phe Tyr  
                     210                      215                      220  
 Ser Arg Gly Leu Asn Ser Leu Glu Ser Thr Leu Thr Phe Pro Ala Ser  
 225                      230                      235                      240  
 Thr Ser Thr Ile Phe  
                     245

&lt;210&gt; 160

&lt;211&gt; 3550

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 160

ccctcgata atggattact aaatgggata cacgctgtac cagttcgctc cgagccccgg 60  
 ccgcctgtcc gtcgatgcac cgaaaagggt gaagtagaga aataaagtct ccccgctgaa 120  
 ctactatgag gtcagaagcc ttgctgctat atttcacact gctacacttt gctggggctg 180  
 gtttcccaaga agattctgag ccaatcagta tttcgcatgg caactataca aaacagtatc 240  
 cgggtgttgt gggccacaag ccaggacgga acaccacaca gaggcacagg ctggacatcc 300  
 agatgattat gatcatgaac ggaaccctct acattgctgc tagggaccat atttatactg 360  
 ttgatataga cacatcacac acsgaagaaa tttattgtag caaaaaactg acatggaaat 420  
 ctagacaggg cgaatgagac acatgcagaa tgaagggaaa acataaggat gagggccaca 480  
 actttattaa agttcttcta aagaaaaacg atgatgcatt gtttgtctgt ggaactaatg 540  
 ccttcaaccc ttctgcaga aactataaga tggatacatt ggaaccattc ggggatgaat 600  
 tcagcggaaat ggccagatgc ccatatgatg ccaaacatgc caacgttgca ctgtttgcag 660  
 atggaaaact atactcagcc acagtactg acttcttgc cattgacgca gtcatttacc 720  
 ggagtcttgg agaaagccct accctgcgga ccgtcaagca cgattcaaaa tgggtgaaag 780  
 aaccatactt tgttcaagcc gtggattacg gagattatat ctacttcttc ttcagggaaa 840  
 tagcagtgga gtataacacc atgggaaagg tagttttccc aagagtgggt caggtttgta 900  
 agaatgatat gggaggatct caaagagtcc tggagaaaca gtggacgtcg ttcttgaagg 960  
 cgcgcttgaa ctgctcagtt cctggagact ctcatTTTTA tttcaacatt ctccaggcag 1020  
 ttacagatgt gattcgtatc aacgggcgtg atgttgtcct ggcaacgttt tctacacctt 1080  
 ataacagcat ccctgggtct gcagtcctgt cctatgacat gcttgacatt gccagtgttt 1140  
 ttactgggag attcaaggaa cagaagtctc ctgattccac ctggacacca gtctctgatg 1200  
 aacgagttcc taagcccagg ccagggtgct gtgctggctc atctctctta gaaagatatg 1260  
 caacctccaa tgagttccct gatgataccc tgaacttcat caagacgcac ccgctcatgg 1320  
 atgaggcagt gccctccatc ttcaacaggg catggttccct gagaacaatg gtcagatacc 1380  
 gccttaccaa aattgcagtg gacacagctg ctggggccata tcagaatcac actgtgggtt 1440  
 ttctgggatc agagaaggga atcatcttga agtttttggc cagaatagga aatagtgggt 1500  
 ttctaataga cagccttttc ctggaggaga tgagtgttta caactctgaa aaatgcagct 1560  
 atgatggagt cgaagacaaa aggatcatgg gcatgcagct ggacagagca agcagctctc 1620  
 tgtatgttgc gttctctacc tgtgtgataa aggttcccc tggccggtgt gaacgacatg 1680  
 ggaagtgtaa aaaaacctgt attgcctcca gagaccata ttgtggatgg ataaaggaag 1740  
 gtggtgcctg cagccattta tcacccaaca gcagactgac ttttgagcag gacatagagc 1800

gtggcaatac agatggtctg ggggactgtc acaattcctt tgtggcactg aatggagtga 1860  
 ttccgggaaag ttacctcaaa ggccacgacc agctggttcc cgtcacccctc ttggccattg 1920  
 cagtcacccct ggctttcgtc atggggggccg tcttctcggg catcacccgtc tactgcgtct 1980  
 gtgatcatcg gcgcaaagac gtggctgtgg tgcagcgcaa ggagaaggag ctcacccact 2040  
 cgcgcggggg ctccatgagc agcgtcacca agctcagcgg cctcttttggg gacactcaat 2100  
 ccaaagaccc aaagccggag gccatcctca cgccactcat gcacaacggc aagctcgcca 2160  
 ctcccggcaa caccggccaag atgctcatta aagcagacca gcaccacctg gacctgacgg 2220  
 cctcccccac cccagagtca accccaacgc tgcagcagaa gcggaagccc agccggcgga 2280  
 gccgcgagtg ggagaggaac cagaacctca tcaatgcctg cacaaggagc atgcccccca 2340  
 tgggctcccc tgtgattccc acggacctgc cctgcgggc ctccccagc cacatcccca 2400  
 gcgtggtggt cctgcccacg acgcagcagg gctaccagca tgagtacgtg gaccagccca 2460  
 aaatgagcga ggtggcccag atggcgctgg aggaccaggc cgccacactg gagtataaga 2520  
 ccatcaagga acatttcagc agcaagagtc ccaaccatgg ggtgaacctt gtggagaacc 2580  
 tggacagcct gcccccaaaa gtccacagc gggaggcctc cctgggtccc ccgggagcct 2640  
 ccctgtttca gaccggttta agcaagcggc tggaaatgca ccactccttt tcctacgggg 2700  
 ttgactataa gaggagctac cccacgaact cgctcacgag aagccaccag gccaccactc 2760  
 tcaaaagaaa caacactaac tcctccaatt cctctcacct ctccagaaac cagagctttg 2820  
 gcaggggaga caaccgcgcg cccgcccgcg agagggtgga ctccatccag gtgcacagct 2880  
 ccagccatc tggccaggcc gtgactgtct cgaggcagcc cagcctcaac gcctacaact 2940  
 cactgacaag gtcggggctg aagcgtacgc cctcgctaaa gccggacgta cccccaaaac 3000  
 catcctttgc tcccccttcc acatccatga agcccaatga tgcgtgtaca taatcccagg 3060  
 gggaggggggt caggtgtcga accagcaggc aaggcgaggt gcccgcctcag ctcagcaagg 3120  
 ttctcaactg cctcgagtac ccaccagacc aagaaggcct gcggcagagc cgaggacgct 3180  
 gggctctcct ctctgggaca cagggtact cagaaaaact gggccgcgtg gtttggtgaa 3240  
 ggtttgcaac ggccggggact cacccttcatt ctcttcttcc actttcccc acaccctaca 3300  
 acaggtcgga cccacaaaag acttcagtta tcatcacaaa catgagccaa aagcacatac 3360  
 ataccctac cccaccccc acacacacac acacatgcac acaacacata cacacacag 3420  
 cacagaggtg aacagaaact gaaacatttt gtccacaact tcacgggagc tggccagact 3480  
 ggggttgcgt tccaacctgc aaaacacaaa tacatttttt aaaatcaaga aaatttaaaa 3540  
 aaaaaaaaaa 3550

&lt;210&gt; 161

&lt;211&gt; 975

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 161

Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala  
 1 5 10 15

Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly  
 20 25 30

Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg  
 35 40 45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met  
 50 55 60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp  
 65 70 75 80

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr  
 85 90 95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys  
 100 105 110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn  
 115 120 125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys  
 130 135 140  
 Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser  
 145 150 155 160  
 Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu  
 165 170 175  
 Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala  
 180 185 190  
 Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg  
 195 200 205  
 Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln  
 210 215 220  
 Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala  
 225 230 235 240  
 Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln  
 245 250 255  
 Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln  
 260 265 270  
 Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp  
 275 280 285  
 Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg  
 290 295 300  
 Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn  
 305 310 315 320  
 Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala  
 325 330 335  
 Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr  
 340 345 350  
 Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys  
 355 360 365  
 Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe  
 370 375 380  
 Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu  
 385 390 395 400  
 Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val  
 405 410 415  
 Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr  
 420 425 430  
 Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu  
 435 440 445



Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu  
 450 455 460  
 Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp  
 465 470 475 480  
 Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser  
 485 490 495  
 Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu  
 500 505 510  
 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser  
 515 520 525  
 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His  
 530 535 540  
 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly  
 545 550 555 560  
 Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn  
 565 570 575  
 Gly Val Ile Arg Glu Ser Tyr Leu Lys Gly His Asp Gln Leu Val Pro  
 580 585 590  
 Val Thr Leu Leu Ala Ile Ala Val Ile Leu Ala Phe Val Met Gly Ala  
 595 600 605  
 Val Phe Ser Gly Ile Thr Val Tyr Cys Val Cys Asp His Arg Arg Lys  
 610 615 620  
 Asp Val Ala Val Val Gln Arg Lys Glu Lys Glu Leu Thr His Ser Arg  
 625 630 635 640  
 Arg Gly Ser Met Ser Ser Val Thr Lys Leu Ser Gly Leu Phe Gly Asp  
 645 650 655  
 Thr Gln Ser Lys Asp Pro Lys Pro Glu Ala Ile Leu Thr Pro Leu Met  
 660 665 670  
 His Asn Gly Lys Leu Ala Thr Pro Gly Asn Thr Ala Lys Met Leu Ile  
 675 680 685  
 Lys Ala Asp Gln His His Leu Asp Leu Thr Ala Leu Pro Thr Pro Glu  
 690 695 700  
 Ser Thr Pro Thr Leu Gln Gln Lys Arg Lys Pro Ser Arg Gly Ser Arg  
 705 710 715 720  
 Glu Trp Glu Arg Asn Gln Asn Leu Ile Asn Ala Cys Thr Lys Asp Met  
 725 730 735  
 Pro Pro Met Gly Ser Pro Val Ile Pro Thr Asp Leu Pro Leu Arg Ala  
 740 745 750  
 Ser Pro Ser His Ile Pro Ser Val Val Val Leu Pro Ile Thr Gln Gln  
 755 760 765

Gly Tyr Gln His Glu Tyr Val Asp Gln Pro Lys Met Ser Glu Val Ala  
 770 775 780  
 Gln Met Ala Leu Glu Asp Gln Ala Ala Thr Leu Glu Tyr Lys Thr Ile  
 785 790 795 800  
 Lys Glu His Phe Ser Ser Lys Ser Pro Asn His Gly Val Asn Leu Val  
 805 810 815  
 Glu Asn Leu Asp Ser Leu Pro Pro Lys Val Pro Gln Arg Glu Ala Ser  
 820 825 830  
 Leu Gly Pro Pro Gly Ala Ser Leu Phe Gln Thr Gly Leu Ser Lys Arg  
 835 840 845  
 Leu Glu Met His His Ser Phe Ser Tyr Gly Val Asp Tyr Lys Arg Ser  
 850 855 860  
 Tyr Pro Thr Asn Ser Leu Thr Arg Ser His Gln Ala Thr Thr Leu Lys  
 865 870 875 880  
 Arg Asn Asn Thr Asn Ser Ser Asn Ser Ser His Leu Ser Arg Asn Gln  
 885 890 895  
 Ser Phe Gly Arg Gly Asp Asn Pro Pro Pro Ala Pro Gln Arg Val Asp  
 900 905 910  
 Ser Ile Gln Val His Ser Ser Gln Pro Ser Gly Gln Ala Val Thr Val  
 915 920 925  
 Ser Arg Gln Pro Ser Leu Asn Ala Tyr Asn Ser Leu Thr Arg Ser Gly  
 930 935 940  
 Leu Lys Arg Thr Pro Ser Leu Lys Pro Asp Val Pro Pro Lys Pro Ser  
 945 950 955 960  
 Phe Ala Pro Leu Ser Thr Ser Met Lys Pro Asn Asp Ala Cys Thr  
 965 970 975

<210> 162  
 <211> 1723  
 <212> DNA  
 <213> Homo sapiens

<400> 162  
 ctgcagactt tggggtcacc ggccagccac acaggcaccg ttttcagatg tccacttctc 60  
 attgggtaca tcaatctttt aacttttgggg gtcacagttt tagccacett tcgggggggtg 120  
 actggagcag taggaggtgt ggggtcattt tatgaatata ataaaatgga gctgactatg 180  
 gacrrrgact wagtgtgggg gagaggggac gatacagggg gtgtgtcttg gtagtccttg 240  
 gggacagggg ccccccggtg gtcctatggc aggatgagaa rggagggact tggctcccc 300  
 agagccccgt ggaagctact gttctctcca gtgtctcgag cgtagccaaa ataagggttg 360  
 gaggtccccg gcctgtctgc tgtgtctga gctggctgca agcccaggtg ggggagcgag 420  
 tctgggaaga ttggctttga ctctctgttg ccagaggaga tgccatccca gcacggcccc 480  
 cactgtagtc caggctctgt gtggcagcgg gggcaagggg aggggcaagg ctgccccccac 540  
 cccacgcacc aagtcacgcc aagtctcagc aggtaaaagc acgtgagcct agggcgagcg 600  
 gagggagtc tgggtggcccc gcagggtcagg agggaaagca gggctcagag ggcacgtgg 660  
 ccccgaggga gggctctacc tgggggtcag gagcaccttg gtcttgatga ttgattgatt 720  
 gatagaatgg agctgggtct gagcctccca ggcttgagct cctgggagtt cttgtgcggt 780

```

gagctgggca gctcctgggt aggtccgggc accaagcagg ccctgatgtg gacagagtcc 840
catcagaggg agctgatgaa gaatgggtccc tgtaagtaag tcactagggt caacaactgc 900
ctggccgagc actcagcccc tggagctcag gccaacacca gagccccggt tttaggggccc 960
aggagagcag gtgaccaatt atttggggag tcttgggtag aatttccgcc acacattctc 1020
cccagggctg caggggtctt ccgaggcagg gcggtggagc aggattcagg atgtggtggg 1080
aatagagtga ggggcagtgg gtgggcagac ctgggcgtca gaggtcctga tgggaaagga 1140
ggcaggggct acccagagag gggggctcgt gtggcacagc cccaccgac tccgccgtcc 1200
ccctccccctg tgagccccgg gggctgtaca tactctactc catccccctg tccatccctg 1260
agaccacccc cggccgcccctt gcgtcgactt agcaaccacc tcataggccc acccacctcg 1320
ggatccgagc caaccatccc acatcacaaa ctttgggttg ggggacttta cgttcgttta 1380
atttctcatt ttgtacggag aaatattctt ttcaaaagcg tcttttgact gaagtaactt 1440
tcctgggtgct gttgttaact cgttcctttt tttaatttat tccccaccc caggcagccc 1500
tcctgggttcc tactcaccct cccccctcc cccaccctcc gtcccatctg aaccatttgt 1560
ttcttttctt tccgtcagat tttggaaaaa ttctctctc ctccccgcc cctccacacc 1620
atctcccccg atttaaatat agtcactgct acaagtaaca gatgcactgt gaagattcca 1680
gtattaataa aggtgtactg taattaacaa aaaaaaaaaa aaa 1723

```

&lt;210&gt; 163

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (49)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (51)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (81)

&lt;400&gt; 163

```

Val Phe Arg Cys Pro Leu Leu Ile Gly Tyr Ile Asn Leu Leu Thr Leu
  1             5             10             15

```

```

Gly Val Thr Val Leu Ala Thr Phe Arg Gly Val Thr Gly Ala Val Gly
      20             25             30

```

```

Gly Val Gly Ser Phe Tyr Glu Tyr Asn Lys Met Glu Leu Thr Met Asp
  35             40             45

```

```

Xaa Asp Xaa Val Trp Gly Arg Gly Asp Asp Thr Gly Cys Val Ser Gly
  50             55             60

```

```

Ser Ala Trp Gly Thr Gly Thr Pro Arg Trp Ser Tyr Gly Arg Met Arg
  65             70             75             80

```

```

Xaa Glu Gly Leu Gly Ser Pro Arg Ala Arg Trp Lys Leu Leu Phe Ser
      85             90             95

```

```

Pro Val Ser Arg Ala
      100

```

&lt;210&gt; 164

&lt;211&gt; 469

&lt;212&gt; DNA

<213> Homo sapiens

<400> 164

```

gcaacataca agccggccat attagagaga tggaaataaa gcttccttaa tgttgatat 60
gtctttgaag tacatccgtg catttttttt tagcatccaa ccattcctcc cttgtagttc 120
tcgccccctc aaatcaccct ctcccgtagc ccaccgcact aacatctcag tctctgaaaa 180
tgcacagaga tgcctggcta cctcgccctg ccttcagcct cacggggctc agtctctttt 240
tctctttggt gccaccagga cggagcatgg aggtcacagt acctgccacc ctcaacgtcc 300
tcaatggctc tgacgcccgc ctgcccgtga ccttcaactc ctgctacaca gtgaaccaca 360
aacagtcttc cctgaactgg acttaccagg agtgcaacaa ctgctctgag gagatgttcc 420
tccagttccg catgaagatc attaacctga agctggagcg gtttcaaga 469

```

<210> 165

<211> 96

<212> PRT

<213> Homo sapiens

<400> 165

```

Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr Gly
 1             5             10             15
Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met Glu Val
                20             25             30
Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp Ala Arg Leu
        35             40             45
Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His Lys Gln Phe Ser
        50             55             60
Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys Ser Glu Glu Met Phe
        65             70             75             80
Leu Gln Phe Arg Met Lys Ile Ile Asn Leu Lys Leu Glu Arg Phe Gln
                85             90             95

```

<210> 166

<211> 454

<212> DNA

<213> Homo sapiens

<400> 166

```

tggcttttgg ctacagagag ggaagggaaa gcctgaggcc ggcataaggg gaggccttgg 60
aacctgagct gccaatgcca gccctgtccc atctgcgccc acgatactcg ctctctctcc 120
aacaactcct ttggtgggga caaaagtgc aattgtaggc caggcacagt ggctcacgcc 180
tgtaatccca gcacttttgg aggccaaaggc ggggtggatta cctccatctg tttagtagaa 240
atggggcaaaa ccccatTTTT actaaaaata caagaattag ctgggcgtgg tggcgtgtgc 300
ctgtaatccc agctatttgg gaggtgagg caggagaatc gcttgagccc gggaagcaga 360
ggttgcagtg aactgagata gtgatagtgc cactgcaatt cagcctgggt gacatagaga 420
gactccatct caaaaaaaaaa aaaaaaaaaa aaaa 454

```

<210> 167

<211> 736

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (680)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (704)

&lt;400&gt; 167

```

gtttttaaac attatgttct acatgataaa tacatataat agtatgtcta tttaaataat 60
taaatTTGaa aaaaactaat caaatattat cataagtaat gataaaaacc acaatttctt 120
ttgcagcaaa ctaataacac ctggatttct caatttatta agttgtactt acctgatgct 180
gatgatgatt actgtattta cacattgtct cagagctcac tcttgccggag gttgtggcct 240
cgaaaatgcc ttgttgcccc tctggaatct gtcttttcag cttcatctcc tcctcctcac 300
ctcctgctgt ggtgcacaga tacctatagg caggctccat ctctcctccc ccagctcctc 360
ccctagtcca cagataccta taggcaggct tcctcctccc ctccccagct tctcccctag 420
tgcaacagata cctataggca ggctccatct cctcctcccc agctcctccc ctartgcaca 480
gacacctata ggcaagctcc atctcctcct ctttagctag cctccccatc tcatacacaac 540
gcattgtctgt gaccttttgt aatcatttac agtgccacac ggaacctgtg attttgcaca 600
cagcaaaaca aacaatgttt agctttatct atggtatttg atgactgtaa atggaaataa 660
atattgttct ttattttttt aaaaaaaaaa aaaaaaaaaa aaanaaaaaa aaaaaaaaaa 720
aaaaaaaaaa aaaaaa                                     736

```

&lt;210&gt; 168

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (100)

&lt;400&gt; 168

```

Met Leu Met Met Ile Thr Val Phe Thr His Cys Leu Arg Ala His Ser
 1             5             10            15

Cys Gly Gly Cys Gly Leu Glu Asn Ala Leu Leu Ser Leu Trp Asn Leu
      20             25            30

Ser Phe Gln Leu His Leu Leu Leu Leu Thr Ser Cys Cys Gly Ala Gln
      35             40            45

Ile Pro Ile Gly Arg Leu His Leu Leu Leu Pro Ser Ser Ser Pro Ser
      50             55            60

Ala Gln Ile Pro Ile Gly Arg Leu His Leu Leu Leu Pro Ser Phe Ser
      65             70            75            80

Pro Ser Ala Gln Ile Pro Ile Gly Arg Leu His Leu Leu Leu Pro Ser
      85             90            95

Ser Ser Pro Xaa Ala Gln Thr Pro Ile Gly Lys Leu His Leu Leu Leu
      100            105            110

Phe Ser

```

&lt;210&gt; 169

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

gtagttacta actccaacac ctaatagcat tggtagaaag cttataaatg cagttattta 60  
 gcctcgacta agatttttct gatacctagt ttcacttttt aatgccctct gaaagttttt 120  
 tgatcagttg tttaatggga gatctgaaat gttaaactca gaccagaaag aagagaacct 180  
 gttttctaga aattaggttt ttaatccaag taagatgcaa gcttttgctt ttttaataac 240  
 ttgtatagct aaaaacttga cggtagaaaag ctctcagatc aaagctgac cttctgtcag 300  
 taatgattct aaaaataaag aagattttta tggggaatat attttatttc attcttatct 360  
 caaacctagg tactgtgggc gttttgagtt catttcgagg cattttcaat gtgcctcagg 420  
 ccacatccaa cctctyccca gggccagatt taatgttcag cctcataaag gttatcatag 480  
 ttttaacatt taagtactat tttgcagtgg gtatatacca aaatttgcta atagtaagat 540  
 aaccttagtt atatatcatt cacgttagtt ctatcttgga ggcaataaac atttcttggt 600  
 caagaaattc atgttctatc ttggaggcaa taaacaaaca ttttttgctt aaaattaggg 660  
 ctaccctatt gtcccttatgt cttttcctga tctgtggtca aacatttttc ttagtcattt 720  
 agaaattttc tatgttggtt taaattttct ttaaatctag aatggagtat gtgaccaata 780  
 ctttcctttg gaatggtag gacatttgaa atagagccca ttctttataa agtataaaat 840  
 atgttttaag ctagtatttt taactaaact tttgagaaac tagattcaca tgcgttgta 900  
 agaaataata cagagacctc tttcgtgtac ctttcacttt gtttccaca cagtgaacat 960  
 ctttcaaaac tgcatacaa tatcataccc aggatactga cactgggtata gctaagatag 1020  
 agaagctttc cacacagaac ttttcttagc acaggggatcc ctcatcttgc ttttgatgac 1080  
 cataccact tcaactccat ccctactccc ttcttaaccc ttggcaacca taatctgttc 1140  
 tccattttta tagttttttt ttttccattt caataaagct gtataactgg aatcataata 1200  
 atatgtaacc ttttgggatt ggcttttttt catttagcat gattttctgg aggttaatcc 1260  
 agcttattat gtgtatcaag tctattgaca ggtacttttt agtgtgaata gaatccata 1320  
 gtatagatgt accacagttt gtttaactgt tcacctgctg agagacattg ggccagtttt 1380  
 tggctactat aaataaagtt gctataaaca aaaaaaaaaa aaaaaaa 1427

&lt;210&gt; 170

&lt;211&gt; 79

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (45)

&lt;400&gt; 170

Met Ile Leu Lys Ile Ser Lys Ile Leu Met Gly Asn Ile Phe Tyr Phe  
 1 5 10 15  
 Ile Leu Ile Ser Asn Leu Gly Thr Val Val Val Leu Ser Ser Phe Arg  
 20 25 30  
 Gly Ile Phe Asn Val Pro Gln Ala Thr Ser Asn Leu Xaa Pro Gly Pro  
 35 40 45  
 Asp Leu Met Phe Ser Leu Ile Lys Val Ile Ile Val Leu Thr Phe Lys  
 50 55 60  
 Tyr Tyr Phe Ala Val Gly Ile Tyr Gln Asn Leu Leu Ile Val Arg  
 65 70 75

&lt;210&gt; 171

&lt;211&gt; 572

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 171

tgcagattct gtggttatac tcaactctca tcccaaagaa tgaaatttac cactctcctc 60  
 ttcttggcag ctgtagcagg ggccctgggc tatgctgaag atgcctcctc tgactcgacg 120

```

gggtctgata ctgcccagga agctgggacc tctaagccta atgaagagat ctcaggtcca 180
gcagaaccag cttcaccccc agagacaacc acaacagccc aggagacttc ggcggcagca 240
gttcaggagg cagccaaggt cacctcaagc aggcagggaac taaacccccct gaaatccata 300
gtggagaaaa gtatcttact aacagaacaa gcccttgcaa aagcaggaaa aggaatgcac 360
ggaggcgtgc caggtggaaa acaattcatc gaaaatggaa gtgaatttgc acaaaaatta 420
ctgaagaaat tcagtctatt aaaaccatgg gcatgagaag ctgaaaagaa tgggatcatt 480
ggacttaaag ccttaaatac cctttagacc cagagytatt aaaacgaaag catccaaaaa 540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 572

```

&lt;210&gt; 172

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 172

```

Met Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu
  1             5             10             15
Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala
             20             25             30
Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala
             35             40             45
Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser
             50             55             60
Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu
             65             70             75             80
Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu
             85             90             95
Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly
             100            105            110
Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu
             115            120            125
Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala
             130            135

```

&lt;210&gt; 173

&lt;211&gt; 1223

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 173

```

ccttggtcca cgtagctggc aaggtcttca ttcacttgcc actgctagtc ttccaaccct 60
tctggacttt ctttgccttt gtcttggttt ggggtgtactg gatcatgaca cttctttttc 120
ttggcactac cggcagtcct gttcagaatg agcaaggcct tgtggagttc aaaatttctg 180
ggcctctgca gtacatgtgg tgggtaccatg tgggtggcct gatttggatc agtgaattta 240
ttctagcatg tcagcagatg acagtggcag gagctgtggg aacatactat ttactaggg 300
ataaaaggaa tttgccattht acacctattht tggcatcagt aaatgcgctt atycgttacc 360
acctagggtac ggtggcaaaa ggatctttca ttatcacatt agtcaaaatt ccgcgaatga 420
tccttatgta tattcacagt cagctcaaag gaaaggaaaa tgcttgtgca cgatgtgtgc 480
tgaaatcttg catttgttgc ctttgggtgc ttgaaaagtg cctaaaattat ttaaatacaga 540
atgcatacac agccacagct atcaacagca ccaacttctg cacctcagca aaggatgcct 600
ttgtcattct ggtggagaat gctttgagag tggctaccat caacacagta ggagatttta 660

```

```

tggtattcct tggcaagggtg ctgatagtct gcagcacagg tttagctggg attatgctgc 720
tcaactacca gcaggactac acagtatggg tgctgcctct gatcatcgct tgccctcttg 780
ctttcctagt cgctcattgc ttctgtgcta tttatgaaat ggtagtggat gtattattct 840
kgkgttttgc cattgawaca aaatacaatg atgggmgcc tggcagagaa ttctatatgg 900
ataaagtgct gatggagttt gtggaaaaca gtaggaaagc aatgaaagaa gctggtaagg 960
gaggcgctgc tgattccaga gagctaaagc cgatgctgaa gaaaagggtga ctgggtctcat 1020
gagccctgaa gaatgaactc agaggaggtt gtttacctga gggtctccca ctcaccagct 1080
gttgagagtc tgcgattatg aagagcagga tcttattact tcaatgaaag catgtaacaa 1140
gtttctcaaa ccaccaacag ccaagtggat ttggtacagt gcggtgtgtc aataaataat 1200
caaaagcaaa aaaaaaaaaa aaa 1223

```

<210> 174  
 <211> 301  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (246)..(247)

<220>  
 <221> UNSURE  
 <222> (251)

<220>  
 <221> UNSURE  
 <222> (258)

<400> 174  
 Met Thr Leu Leu Phe Leu Gly Thr Thr Gly Ser Pro Val Gln Asn Glu  
 1 5 10 15  
 Gln Gly Phe Val Glu Phe Lys Ile Ser Gly Pro Leu Gln Tyr Met Trp  
 20 25 30  
 Trp Tyr His Val Val Gly Leu Ile Trp Ile Ser Glu Phe Ile Leu Ala  
 35 40 45  
 Cys Gln Gln Met Thr Val Ala Gly Ala Val Val Thr Tyr Tyr Phe Thr  
 50 55 60  
 Arg Asp Lys Arg Asn Leu Pro Phe Thr Pro Ile Leu Ala Ser Val Asn  
 65 70 75 80  
 Arg Leu Ile Arg Tyr His Leu Gly Thr Val Ala Lys Gly Ser Phe Ile  
 85 90 95  
 Ile Thr Leu Val Lys Ile Pro Arg Met Ile Leu Met Tyr Ile His Ser  
 100 105 110  
 Gln Leu Lys Gly Lys Glu Asn Ala Cys Ala Arg Cys Val Leu Lys Ser  
 115 120 125  
 Cys Ile Cys Cys Leu Trp Cys Leu Glu Lys Cys Leu Asn Tyr Leu Asn  
 130 135 140  
 Gln Asn Ala Tyr Thr Ala Thr Ala Ile Asn Ser Thr Asn Phe Cys Thr  
 145 150 155 160  
 Ser Ala Lys Asp Ala Phe Val Ile Leu Val Glu Asn Ala Leu Arg Val



165	170	175
Ala Thr Ile Asn Thr Val Gly Asp Phe Met Leu Phe Leu Gly Lys Val		
180	185	190
Leu Ile Val Cys Ser Thr Gly Leu Ala Gly Ile Met Leu Leu Asn Tyr		
195	200	205
Gln Gln Asp Tyr Thr Val Trp Val Leu Pro Leu Ile Ile Val Cys Leu		
210	215	220
Phe Ala Phe Leu Val Ala His Cys Phe Leu Ser Ile Tyr Glu Met Val		
225	230	235
Val Asp Val Leu Phe Xaa Xaa Phe Ala Ile Xaa Thr Lys Tyr Asn Asp		
245	250	255
Gly Xaa Pro Gly Arg Glu Phe Tyr Met Asp Lys Val Leu Met Glu Phe		
260	265	270
Val Glu Asn Ser Arg Lys Ala Met Lys Glu Ala Gly Lys Gly Gly Val		
275	280	285
Ala Asp Ser Arg Glu Leu Lys Pro Met Leu Lys Lys Arg		
290	295	300

<210> 175  
 <211> 2460  
 <212> DNA  
 <213> Homo sapiens

<400> 175  
 gagaagcgcg atgacgggcta cgaggccgct gccagctcca aaactagctc aggcgatgcc 60  
 tcttcactca gcatcgaggg agactaacia actccgggca aagttggggc tgaaccctt 120  
 ggagggttaat gccatcaaga aggagggcggg caccaggag gagcccgta cagctgatgt 180  
 catcaacctt atggccttgc gacagcgaga ggagctgcgg gagaagctgg cggctgccaa 240  
 ggagaagcgc ctgtcgaacc aaaagctggg gaagataaag accctaggag aggatgacct 300  
 ctggctggac gacactgcag cctggatcga gaggagccgg cagctgcaga aggagaagga 360  
 cctggcagag aagagggcca agttactgga ggagatggac caaaagtgtg gtgtcagcac 420  
 tctggtggag gaggagtctg ggcagaggcg gcaggacctg tacagtgcgc gggacctgca 480  
 gggcctcact gtggagcatg ccattgattc cttccgagaa ggggagacaa tgattcttac 540  
 cctcaaggac aaaggcgtgc tgcaggagga ggaggacgtg ctggtgaacg tgaacctggt 600  
 ggataaggag cgggcagaga aaaatgtgga gctgcggaag aagaagcctg actacctgcc 660  
 ctatgccgag gacgagagcg tggacgacct ggcgcagcaa aaacctcgct ctatcctgtc 720  
 caagtatgac gaaaagcttg aaggggagcg gccacattcc ttccgcttgg agcaggggcg 780  
 cacggctgat ggcctgcggg agcgggagct ggaggagatc cgggccaagc tgcggctgca 840  
 ggctcagtc ctgagcacag tggggccccg gctggcctcc gaataacctca cgcctgagga 900  
 gatggtgacc tttaaaaaaga ccaagcggag ggtgaagaaa atccgcaaga aggagaagga 960  
 ggtagtagtg cgggcagatg acttgctgcc tctcggggac cagactcagg atggggactt 1020  
 tggttccaga ctgcggggac ggggtcgccg ccgagtgtcc gaagtggagg aggagaagga 1080  
 gcctgtgcct cagcccctgc cgtcggacga cacccgagtg gagaacatgg acatcagtga 1140  
 tgaggaggaa ggtggagctc caccgccggg gtccccgcag gtgctggagg aggacgaggc 1200  
 ggagctggag ctgcagaagc agctggagaa gggacgcgg ctgcgacagt tacagcagct 1260  
 acagcagctg cgagacagt gcgagaaggt ggtggagatt gtgaagaagc tggagtctcg 1320  
 ccagcggggc tgggaggagg atgaggatcc cgagcggaag ggggccatcg tgttcaacgc 1380  
 cacgtccgag ttctgccgca ccttggggga gatccccacc tacgggctgg ctggcaatcg 1440  
 cgaggagcag gaggagctca tggactttga acgggatgag gagcgctcag ccaacgggtg 1500  
 ctccgaatct gacggggagg agaacatcgg ctggagcacg gtgaacctgg acgaggagaa 1560  
 gcagcagcag gatgtgaggg ccacgccgct ggggggtggg cgtttggggg tgctcaagct 1620

ggagatgagc accgggctcg gtgtccagag cctcagcctc ctcattccaga gtgggctctg 1680  
 cagacctccc agggcgatct gaggagtaaa tgaggaaatt aaatgttgtg gagggctggt 1740  
 gcctggcagg tgggtgaccag tgggtggggc tgagaagagc cggtagggcc tgctaaccac 1800  
 ccccgccacg tgtcccgtag ttctctgctt cctccaccac catcctggac gaggaaccga 1860  
 tcgtgaatag ggggctggca gctgccctgc tctgtgtca gaacaaaggg ctgctggaga 1920  
 ccacagtga gaaggtggcc cgggtgaagg cccccaacaa gtcgctgccc tcagccgtgt 1980  
 actgcatcga ggataagatg gccatcgatg acaagtacag cgggagggag gaataccgag 2040  
 gcttcacaca ggacttcaag gagaaggacg gtacaaaccc gacgttaaga tcgaatacgt 2100  
 ggatgagacg ggccggaaac tcacacccaa ggaggctttc cggcagctgt cgcaccgctt 2160  
 ccatggcaag ggctcaggca agatgaagac agagcggcgg atgaagaagc tggacgagga 2220  
 ggcgctcctg aagaagatga gctccagsga caccgccytg ggcaccgtgg cctgytcca 2280  
 ggagaagcag aaggctcaga agaccccta catygtgttc agcggcagcg gcaagagcat 2340  
 gaacgcgaac accatcacca agtgacagcg cctcccgcc cgggcccctgc ctcaaccttc 2400  
 atattaaata agctccctc cttaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 2460

<210> 176

<211> 563

<212> PRT

<213> Homo sapiens

<400> 176

Met Thr Ala Thr Arg Pro Leu Pro Ala Pro Lys Leu Ala Gln Ala Met  
1 5 10 15

Pro Pro His Ser Ala Ser Arg Glu Thr Asn Lys Leu Arg Ala Lys Leu  
20 25 30

Gly Leu Lys Pro Leu Glu Val Asn Ala Ile Lys Lys Glu Ala Gly Thr  
35 40 45

Lys Glu Glu Pro Val Thr Ala Asp Val Ile Asn Pro Met Ala Leu Arg  
50 55 60

Gln Arg Glu Glu Leu Arg Glu Lys Leu Ala Ala Lys Glu Lys Arg  
65 70 75 80

Leu Leu Asn Gln Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu Asp Asp  
85 90 95

Pro Trp Leu Asp Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg Gln Leu  
100 105 110

Gln Lys Glu Lys Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu Glu Glu  
115 120 125

Met Asp Gln Lys Phe Gly Val Ser Thr Leu Val Glu Glu Glu Phe Gly  
130 135 140

Gln Arg Arg Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly Leu Thr  
145 150 155 160

Val Glu His Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met Ile Leu  
165 170 175

Thr Leu Lys Asp Lys Gly Val Leu Gln Glu Glu Asp Val Leu Val  
180 185 190

Asn Val Asn Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val Glu Leu  
195 200 205

Arg Lys Lys Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu Ser Val  
 210 215 220  
 Asp Asp Leu Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys Tyr Asp  
 225 230 235 240  
 Glu Lys Leu Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu Gln Gly  
 245 250 255  
 Gly Thr Ala Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile Arg Ala  
 260 265 270  
 Lys Leu Arg Leu Gln Ala Gln Ser Leu Ser Thr Val Gly Pro Arg Leu  
 275 280 285  
 Ala Ser Glu Tyr Leu Thr Pro Glu Glu Met Val Thr Phe Lys Lys Thr  
 290 295 300  
 Lys Arg Arg Val Lys Lys Ile Arg Lys Lys Glu Lys Glu Val Val Val  
 305 310 315 320  
 Arg Ala Asp Asp Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp Gly Asp  
 325 330 335  
 Phe Gly Ser Arg Leu Arg Gly Arg Gly Arg Arg Arg Val Ser Glu Val  
 340 345 350  
 Glu Glu Glu Lys Glu Pro Val Pro Gln Pro Leu Pro Ser Asp Asp Thr  
 355 360 365  
 Arg Val Glu Asn Met Asp Ile Ser Asp Glu Glu Glu Gly Gly Ala Pro  
 370 375 380  
 Pro Pro Gly Ser Pro Gln Val Leu Glu Glu Asp Glu Ala Glu Leu Glu  
 385 390 395 400  
 Leu Gln Lys Gln Leu Glu Lys Gly Arg Arg Leu Arg Gln Leu Gln Gln  
 405 410 415  
 Leu Gln Gln Leu Arg Asp Ser Gly Glu Lys Val Val Glu Ile Val Lys  
 420 425 430  
 Lys Leu Glu Ser Arg Gln Arg Gly Trp Glu Glu Asp Glu Asp Pro Glu  
 435 440 445  
 Arg Lys Gly Ala Ile Val Phe Asn Ala Thr Ser Glu Phe Cys Arg Thr  
 450 455 460  
 Leu Gly Glu Ile Pro Thr Tyr Gly Leu Ala Gly Asn Arg Glu Glu Gln  
 465 470 475 480  
 Glu Glu Leu Met Asp Phe Glu Arg Asp Glu Glu Arg Ser Ala Asn Gly  
 485 490 495  
 Gly Ser Glu Ser Asp Gly Glu Glu Asn Ile Gly Trp Ser Thr Val Asn  
 500 505 510  
 Leu Asp Glu Glu Lys Gln Gln Gln Asp Val Arg Ala Thr Pro Leu Gly  
 515 520 525

Gly Gly Arg Leu Gly Val Leu Lys Leu Glu Met Ser Thr Gly Leu Gly  
530 535 540

Val Gln Ser Leu Ser Leu Leu Ile Gln Ser Gly Leu Cys Arg Pro Pro  
545 550 555 560

Arg Ala Ile

<210> 177

<211> 1790

<212> DNA

<213> Homo sapiens

<400> 177

```

ctgggtaccca cccctgtctc tggacttctt tatgaacact gagtatttga ctccccaccc 60
ttcatgggtca gctcctttta acaccctaga tatcattgct gtccttttca ttgacatgct 120
agagacatttt ccaattttta tgggagtcag taagatagag atgatgaaaa ttcagagtgt 180
tcaaagaaag aggaggcctc atcagttgat agaataatac acagattgtc taatctcagt 240
tttcttcact tttctaccca ttacagtggg aaaaagaacc cttagggaag ccagtgcctc 300
tcaacattgg ttacaaaacc atcagtgcga gcacttaatt taaaatcttc tgaaaatcca 360
tcagttgggt ttcatgtctc actctaaact cagctccaac caggctgctt cctagattct 420
tgctgtgtgt tggttctgtt ttggctcttt gttacttctt tctgtaaact taagtaaact 480
cagtttggtt acctagttaa ttgattcttt ccattttcta tactattcac cagcatatca 540
aagatgcttc ttcttaactc tgatttccag agtaactgtg ctatcagctt ttcataactaa 600
gaactagggt tttacctttt cacatttctt gcttcctacc cagttcgtaa gccaaattag 660
actcgtactc ttgtgaagtg ccttttagat actagtgtaa aatatactgc gtaattctcc 720
attgccctac atatatatac cctttaagaa aatatatcac cagtctatct tatcttcgca 780
gaacttgccc aggtatgagc cagcatttat taccactcat tctagaaggt gccagttagg 840
tagctatcca ggtttacatt ttaaggcagt cgagacctta ttcacgtggt atataaaca 900
ccacatttct cttttatatg gaacaagact tttcatttgc ggctggcctt ctcactagct 960
tatgcttttt ttttttaaga cctttcttag cactcgtgta actcctcccc ctcacaatca 1020
atctcagcaa ctcagcagag tcgcttcagt tcacagctct taatccttca ctcagacta 1080
aagctaactc tatgtcctca aacagctaca actcactgtt atcacagttc cgactgcaga 1140
gactccattt aagaggaaat ttaaaaaata aacaatgctc tatttctgtc cacatcaaa 1200
gtacctctaa cagaaacttg tctttgcttc tgtctctctg ctactggact ctcagctcaa 1260
ggtaatgtaa gatgatctca tagatgcact ttagcctctt gatgttagca gttgagtcct 1320
ccctgcgcac aaaatacatt tgtggtaatg aatgccaga atctcactgg cacacccaag 1380
agtagttaaa ctaaaattgc tactaacaca acattgtaga attcgttgcc ttaatggatg 1440
tgatcttcta ggcttactgt gtcttaacaa gcagtcttat atatatatat cttgcccaga 1500
aagtacactt gtagaattta acatttgctc ttttctccaa acagattaaa gggtatgcag 1560
ctgaatgatt ctgtgtccca ttttaaaggc ccaggctatc ccctagattt agattagttc 1620
ctaaaaaatc ttccagtctg aatcctgaca aatggatagc taaattaatt tccactctc 1680
ttctctcttg cactgtttgg tacattacag ccaccattag ccttaaaagc tgcagcagcc 1740
aaattcgggt acagtaacat aaagcctgag cttaaaaaaa aaaaaaaaaa 1790

```

<210> 178

<211> 115

<212> PRT

<213> Homo sapiens

<400> 178

Met Glu Gln Asp Phe Ser Phe Ala Ala Gly Leu Leu Thr Ser Leu Cys  
1 5 10 15

Phe Phe Phe Leu Arg Pro Phe Leu Ala Leu Ala Glu Leu Leu Pro Leu  
20 25 30

Thr Ile Asn Leu Ser Asn Ser Ala Glu Ser Leu Gln Phe Thr Ala Leu

35

40

45

Asn Pro Ser Leu Gln Thr Lys Ala Asn Leu Met Ser Ser Asn Ser Tyr  
50 55 60

Asn Ser Leu Leu Ser Gln Phe Arg Leu Gln Arg Leu His Leu Arg Gly  
65 70 75 80

Asn Leu Lys Asn Lys Gln Cys Ser Ile Ser Val His Ile Lys Gly Thr  
85 90 95

Ser Asn Arg Asn Leu Ser Leu Leu Leu Ser Leu Cys Tyr Trp Thr Leu  
100 105 110

Ser Ser Arg  
115

&lt;210&gt; 179

&lt;211&gt; 2026

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 179

cattgagttg ccctaacaac attgtctcca gtgtcagaac catattaag ttcgtttctc 60  
agattgggag cctgcaacac catacagcca acattgcctt tgccacgcca ctgccaccat 120  
ccccaccatt gccctatggt gggcagatga attccagaaa ccctcaggga gccaggataa 180  
ttaggcaacc catctgaatt ggccacgtaa gtgacaggca cttatctctc gggttctctg 240  
ttttgcagac tccagggaag tcctgtctag aggtcgatgg cagagactcc tactctttcc 300  
catgaggggt tgataggaat caaattggga ttcttttggc ttggggtttt gttttttgt 360  
tgttgttttt ggttttcagt ttgttttttg gtgtatgggg ggtgatattg tttctgaata 420  
agaaaaagaa gaggcaacca tggcccttat gtgggttat cttttttgag caatgtttta 480  
gccacaagta agaatcttg aaagtctttt gtccagcaag cagtcttaaa aatgtttttc 540  
ctaactcctt ttgcagggtga ctaagtacaa aaaaatagtt ttctcattgt attcaaaata 600  
gtgagtaggt tccttgata atacacagtg gtagttgaca tttttttca aaacacaacc 660  
agaaaacca cttccggtat ttgtaaatca cttttcaagg gaaaaagtga acacgtattc 720  
cttgattttc tagtttgatt accaaacctg atgttacaaa gaaacctccg ttctgtagac 780  
agaattttct ttatttttct tcttttactc ctcaaatca ctttccaggt gccatcacca 840  
tctataaggt ctccagcag aggtattatc atggtataa gtgggggtgt ggtgcagcca 900  
ttccagtaac acccacaaga ggacagctgt tctgaatgtc cccaccacc cctctttcag 960  
tacaggtgag acattttcag ttcatgagct ccagaccaa tcccaggcca gcccttgac 1020  
caaaagcctt ttttagaagg cttatcagtc cattaggaat gtctcaggaa agatgagcca 1080  
tttctttggg gagaaatata ttacagatg gaagtgtgt actgcgtgtc tgtgtgtgtg 1140  
tgtggtgtgt gtgcgcagct gagtgcgtgt gttcatctat gtgcatttca cttccataaa 1200  
gacccagccc aagctgctgg gaaccatgtg ttcttgagta ttctcagagg ttaaacaaagt 1260  
gacaagttag cttctgaaat tagtgtctca gcaagctggc tttaggaatg agccccattt 1320  
tatcaagcag agaaaaaaaa taacagcaga aaagataaag ataaaccaa aatatatacc 1380  
ccccaatgga aaataatggt gattcagcaa ttcccatagg atgtattaca tgctctaatt 1440  
tattatatta ttatttatct gtctttgatc ttgcccatt gtactcttaa aaagatgttg 1500  
ggatgttgat tgcgattttt aaacaactag ataatgtata aatcagcagt ggaaatcagt 1560  
tttaatgtgt ggatgtgtct gattattggt aaatgcctct ttttttactt tttttttttt 1620  
tagatgtata atgtttcata aacctggca ctgggcacaa agctcagctg tgaaaatgaa 1680  
atgtgtagta tttttaaaca tgaatgtcaa tttcaagtgt atttgaaatg gttcctccag 1740  
gagagatatt tgtgcacat taggaaaatc ttctctgcag aggaagtgc cttctttgga 1800  
gaaaatggaa aatgggttct gatattgtat ctccagtag cccatttctt agggcaccat 1860  
ggaaaacaca aatgtgatct ttaagtatac ctcttcccca gtttggggag gaaaggactc 1920  
agtttgcacc ctttttgtat gtaaaataaa atgtcttacc tttcttggtt aaaaaaaa 1980  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2026

&lt;210&gt; 180

<211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Met Leu Gln Arg Asn Leu Arg Ser Val Asp Arg Ile Ser Phe Ile Phe  
 1 5 10 15  
 Leu Leu Leu Leu Leu Thr Ile Thr Phe Pro Val Pro Ser Pro Ser Ile  
 20 25 30  
 Arg Ser Gln Ser Arg Gly Leu Phe Met Val Ile Ser Gly Gly Val Val  
 35 40 45  
 Gln Pro Phe Gln  
 50

<210> 181  
 <211> 1138  
 <212> DNA  
 <213> Homo sapiens

<400> 181  
 gggctctgtgg agagccgggt gcgagcggcg gcagcacgag gggaaaagag ctgagcggag 60  
 accaaagtca gccgggagac agtgggtctg tgagagaccg aatagagggg ctggggccac 120  
 gagcgccatt gacaagcaat ggggaagaaa cagaaaaaca agagcgaaga cagcaccaag 180  
 gatgacattg atcttgatgc cttggctgca gaaatagaag gagctggtgc tgccaaagaa 240  
 caggagcctc aaaagtcaaa agggaaaaag aaaaaagaga aaaaaagca ggactttgat 300  
 gaagatgata tcctgaaaga actggaagaa ttgtcttttg aagctcaagg catcaaagct 360  
 gacagagaaa ctgttgacgt gaagccaaca gaaacaatg aagaggaatt cacctcaaaa 420  
 gataaaaaaa agaaggaca gaagggcaaa aaacagagtt ttgatgataa tgatagcgaa 480  
 gaattgggaag ataaagattc aaaatcaaaa aagactgcaa aaccgaaagt ggaaatgtac 540  
 tctgggagtg atgatgatga tgattttaac aaacttccta aaaaagctaa agggaaagct 600  
 caaaaatcaa ataagaagtg ggatgggtca gaggaggatg aggataacag taaaaaaatt 660  
 aaagagcggt caagaataaa ttcttctggt gaaagtgtg atgaatcaga tgaatttttg 720  
 caatctaaaa ggacagaaaa aaaatcagaa aaacaagcca ggtcctaaca tagaaagtgg 780  
 gaatgaagat gatgacgcct ctttcaaaa taagacagtg gcccacaaaga aggcagaaaa 840  
 gaaggagcgc gagagaaaaa agcgagatga agaaaaagcg aaactgcgga agctgaaaga 900  
 aaaagaagag ttagaacacag gtaaaaaagga tcagagttaa caaaaggaat ctcaaaggaa 960  
 atttgaagaa gaaactgtaa aatccaaagt gactgttgat actggagtaa ttctgcctc 1020  
 tgaagagaaa gcagagactc ccacagctgc agaagatgac aatgaaggag acaaaaagaa 1080  
 gaaagataag aagaaaaaga aaggagaaaa ggaagaaaaa gagaaaaaaa aaaaaaaa 1138

<210> 182  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 182  
 Met Gly Lys Lys Gln Lys Asn Lys Ser Glu Asp Ser Thr Lys Asp Asp  
 1 5 10 15  
 Ile Asp Leu Asp Ala Leu Ala Ala Glu Ile Glu Gly Ala Gly Ala Ala  
 20 25 30  
 Lys Glu Gln Glu Prc Gln Lys Ser Lys Gly Lys Lys Lys Lys Glu Lys  
 35 40 45  
 Lys Lys Gln Asp Phe Asp Glu Asp Asp Ile Leu Lys Glu Leu Glu Glu

50                      55                      60  
 Leu Ser Leu Glu Ala Gln Gly Ile Lys Ala Asp Arg Glu Thr Val Ala  
 65                      70                      75                      80  
 Val Lys Pro Thr Glu Asn Asn Glu Glu Glu Phe Thr Ser Lys Asp Lys  
 85                      90                      95  
 Lys Lys Lys Gly Gln Lys Gly Lys Lys Gln Ser Phe Asp Asp Asn Asp  
 100                      105                      110  
 Ser Glu Glu Leu Glu Asp Lys Asp Ser Lys Ser Lys Lys Thr Ala Lys  
 115                      120                      125  
 Pro Lys Val Glu Met Tyr Ser Gly Ser Asp Asp Asp Asp Asp Phe Asn  
 130                      135                      140  
 Lys Leu Pro Lys Lys Ala Lys Gly Lys Ala Gln Lys Ser Asn Lys Lys  
 145                      150                      155                      160  
 Trp Asp Gly Ser Glu Glu Asp Glu Asp Asn Ser Lys Lys Ile Lys Glu  
 165                      170                      175  
 Arg Ser Arg Ile Asn Ser Ser Gly Glu Ser Gly Asp Glu Ser Asp Glu  
 180                      185                      190  
 Phe Leu Gln Ser Lys Arg Thr Glu Lys Lys Ser Glu Lys Gln Ala Arg  
 195                      200                      205

Ser

<210> 183  
 <211> 912  
 <212> DNA  
 <213> Homo sapiens

<400> 183  
 atccagctct ttcagagaga agagatggga ataagataag aacatcattt cctgaagagt 60  
 ttactaagtt gatgttttct tttggtgaag ggcaatgtgg aattttaa atagatttca 120  
 tgtgtgcacc tgtcctgcag tttgaggcag atgattttta accagcatct atagacactt 180  
 cctgtgaagg agagcttcaa gttggcaaag gagatgaagt cacaattaca ctgccacata 240  
 tccctagctg agggcagcag taaaatccag gcccgaaatgg aacagcagcc cactcgctct 300  
 ccacagacgt cacagccacc accacctcca ccacctatgc cattcagagc tccaacgaag 360  
 cctccagttg gacccaaaac ttctcccttg aaagataacc cgtcacctga acctcagttg 420  
 gatgacatca aaagagagct gagggctgaa gttgacatta ttgaacaaat gagcagcagc 480  
 agtgggagca gctcttcaga ctctgagagc tcttcgggaa gtgatgacga tagctccagc 540  
 agtggaggsg aggamaatgg cccagcytct cytccgcagc yttmacacca gcagccytac 600  
 aacagtaggc ctgccgttgc caatggaacc agccggccac aagggaagcaa ccagytyatg 660  
 aacaccctca gaaatgactt gcagttgagt gagtytgga gtgacagtga tgactagtgc 720  
 tggatytttc gaaacctact ttttgggtgca caaacatgcc gcaagactga gctacttttg 780  
 ccgtggagtc cattgcaaga ggaatgtt atggatcagt gactgtagta ggagtttgag 840  
 gctytggaac tctcacatat tcaagtcttt aacttagtgg tgatgggtga aaaaaaaaaa 900  
 aaaaaaaaaa aa 912

<210> 184  
 <211> 167  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (114)

<220>  
 <221> UNSURE  
 <222> (120)

<220>  
 <221> UNSURE  
 <222> (123)..(124)

<220>  
 <221> UNSURE  
 <222> (148)

<220>  
 <221> UNSURE  
 <222> (161)

<400> 184  
 Met Lys Ser Gln Leu His Cys His Ile Ser Leu Ala Glu Gly Ser Ser  
 1 5 10 15  
 Lys Ile Gln Ala Arg Met Glu Gln Gln Pro Thr Arg Pro Pro Gln Thr  
 20 25 30  
 Ser Gln Pro Pro Pro Pro Pro Pro Pro Met Pro Phe Arg Ala Pro Thr  
 35 40 45  
 Lys Pro Pro Val Gly Pro Lys Thr Ser Pro Leu Lys Asp Asn Pro Ser  
 50 55 60  
 Pro Glu Pro Gln Leu Asp Asp Ile Lys Arg Glu Leu Arg Ala Glu Val  
 65 70 75 80  
 Asp Ile Ile Glu Gln Met Ser Ser Ser Ser Gly Ser Ser Ser Ser Asp  
 85 90 95  
 Ser Glu Ser Ser Ser Gly Ser Asp Asp Asp Ser Ser Ser Ser Gly Gly  
 100 105 110  
 Glu Xaa Asn Gly Pro Ala Ser Xaa Pro Gln Xaa Xaa His Gln Gln Pro  
 115 120 125  
 Tyr Asn Ser Arg Pro Ala Val Ala Asn Gly Thr Ser Arg Pro Gln Gly  
 130 135 140  
 Ser Asn Gln Xaa Met Asn Thr Leu Arg Asn Asp Leu Gln Leu Ser Glu  
 145 150 155 160  
 Xaa Gly Ser Asp Ser Asp Asp  
 165

<210> 185  
 <211> 4582  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 185

```

gggtgaagcta atcaaatctg gttcctatgt agctctcact gttcagggac gccacacctg 60
gtcgccccag attccacttg ccgactctga agtagagccg tcagtcattg gacatatgtc 120
tcccacatg acatctcctc attcacctgg agcatctggg aatatggaga gaactactag 180
tctgtgtctc atggggggagg aaaacaatgt ggttcataac cagaaagtag aaattctgag 240
aaaaatgtta cagaaagaac aggaacggct acagttattg caggaagatt acaaccgaac 300
acctgccccaa agattgctaa aagagatcca agaggccaag aaacacattc ctcagctgca 360
agagcagtta tccaaagcca caggctctgc tcaggatgga gctgtagtta caccctccag 420
acctttaggg gacaccctaa cagtcagtga ggcagaaaca gatcctggag atgtactggg 480
caggactgac tgtagcagtg gagatgcttc tcggccagc agtgacaatg cagatagtcc 540
caagagtggc ccaaaagaga gaatttatct agaggaaaac ccagagaaaa gtgaacaat 600
tcaggacact gacactcaat cacttgctcg aagtccctca acccgtag caccctcat 660
tattggagca gaagatgatg attttggtac tgaacatgaa cagatcaatg gacagtgcag 720
ctgtttccag agcattgaat tactaaaatc tcgcccggct catttggtg tttctctaca 780
ccatgtagtt tcacaatttg accctgcgac tttgctctgt tatctctatt cagacctgta 840
taaacatacc aattccaaag aaactcgtcg catcttctct gagttctatc agttctttct 900
aaatcgatca gcacacctga aagtttctgt tctgtatgaa atgtctgcag atctagaaaa 960
gagaagacct gagctcattc ctgaggatct gcatcgccac tatatccaaa ctatgcaaga 1020
aagagtccat ccagaagttc aaaggcactt aaaagatttt cggcagaaac gtagtatggg 1080
actgaccttg gctgaaagcg agctgactaa acttgatgca gagcgagaca aggaccgatt 1140
gactttggag aaggagcggg catgtgcaga acagattgtt gccaaaattg aagaagtatt 1200
gatgaytgct caggctgtar aggaagataa gagctccacc atgcagtatg ttattctcat 1260
gtatatgaag catttgggag taaaagtga agagcctcga aatttggagc acaaacgggg 1320
tcggattgga tttcttccca aaatcaagca aagtatgaag aaagataaag aaggggaga 1380
aaaagggag cgaagaggat tccccagcat cctgggaccc ccacggagac caagccgtca 1440
tgacaacagt gcaattggca gagccatgga actacagaag gcgcgccacc ctaagcact 1500
atccacaccc tcatctgtga gtcctgaacc tcaggacctt gccaaagtgc gccagagtgg 1560
gttagcaaat gaaggaaacag acgctggata cctgcctgcc aattccatgt cttctgtagc 1620
ttcaggggcc tcttttccc aggaaggagg gaaagagaat gatacaggat caaagcaagt 1680
tgagaaaca tcagcacctg gagacacctt agatggcaca cctcgtactc tcaatactgt 1740
ctttgatttc ccaccacctc cattagacca agtgcaggag gaggaatgtg aagtagaaa 1800
gggtgactgaa catgggacac caaagccctt tcgaaagtgt gacagtgtag cttttggaga 1860
aagtcaaagt gaggatgaac aatttgaaaa tgacttagag acagatccac ccaactggca 1920
gcagcttgtt agtcgagaag tgttactggg actaaaacct tgtgaaatca aaagacagga 1980
agtgattaat gaattgttct acactgaaag agctcatgtt cgaacactga aggttcttga 2040
tcaagtgttc tatcagcgag tatccagaga aggaattctg tcaccctcag agctacggaa 2100
aattttttca aacttggaag atattcttca acttcatact ggattgaatg aacaaatgaa 2160
ggctgttcga aagagaaatg agacctctgt tatcgatcag attggggaag atttctgtac 2220
atggttcagc ggaccaggag agggaaaatt gaaacatgct gctgctacct tttgcagtaa 2280
ccaacctttc gccctggaaa tgatcaaatc tcgtcagaaa aaggattctc gatttcagac 2340
ttttgtgcaa gatgctgaaa gtaatccact gtgtcgtcgt cttcaactga aggatattat 2400
tcccactcaa atgcaaaggc ttactaagta cccacttctg ttggataata ttgccaaata 2460
cacagaatgg ccaacagaaa gggagaaggt gaagaaagct gcagatcact gtcgtcagat 2520
cttaaatat gttaatcagg ctgtcaagga ggcagaaaac aagcagcgcc tagaagatta 2580
tcagcgtcgc cttgatacct ccagcctgaa gttgtcagag taccctaatg ttgaagagct 2640
caggaatttg gatttaacaa aaaggaagat gattcatgaa gggccattgg tttggaaggt 2700
gaatagagat aaaactattg atttatcac gttgctgctg gaagacattc ttgtattgtt 2760
acaaaagcag gatgatagac tggttttaag gtgtcatagt aagattctgg catctacagc 2820
tgatagcaaa cacacgttta gccctgtcat taagttgagt acagtgttgg ttcgacaagt 2880
ggcaacagat acaaaagctt tattcgtcat ttccatgtca gacaatggcg ctcagattta 2940
tgaactggg gcacagacag tttctgaaaa gactgtctgg caggacctaa tctgtcggat 3000
ggctgcatca gtgaaggagc aatccacaaa gccgattcca ttaccacagt caacacctgg 3060
cgaaggagat aatgatgaag aagatccttc aaaattaaaa gaggagcagc atggcatttc 3120
agtcactggt ttgcagagtc cagacagaga tttgggarta gaatctacct taatatcgtc 3180
aaaacctcag tctcattcac tgagtacctc tgggaaatca gaggtaactg atctgtttgt 3240
ggctgagaga cagtttgcaa aggaacaaca tacagatggg aactaaagg aagttggaga 3300
agattatcaa atcgcaatcc cagattcaca cctgcctgtc tcagaagaac ggtgggcatt 3360
ggatgcacta agaaatttg gtttgttgaa gcagttgtg gtgcaacagc taggtttgac 3420
tgagaagagc gttcaggaa actggcaaca tttcccaaga tacagaacag cctctcaggg 3480

```

gccgcagaca gacagtgtca tccagaactc tgaaaatatt aaggcctatc attctggtga 3540  
 aggacatatg cccttttagaa ctggaactgg tgacattgca acttggtaca gtccacggac 3600  
 ttcaactgaa tcttttgctc cacgggattc agtgggactg gcaccccagg atagccaggc 3660  
 aagtaacatt ttagtaatgg accacatgat tatgacccca gagatgccta ccatggagcc 3720  
 agaagggggc cttgatgaca gtggagagca cttttttgat gcccggaag cacatagtga 3780  
 tgagaatcca tcagaagggtg atggagcagt taacaaggaa gagaaggatg ttaatttacg 3840  
 catctcagga aactatattga tccttgatgg ctatgaccca gtgcaggaga gttccacaga 3900  
 tgaggagggt gcttcctcac ttaccctgca gcccatgaca ggcatccctg ctgtggaatc 3960  
 caccaccag cagcaacatt ctctcagaa tactactcc gatggggcaa tttcaccatt 4020  
 cacccccga tttctgggtc agcagcgctg gggagctatg gagtattcct gttttgagat 4080  
 ccagagtccc tctctttgtg cagattcaca gagccagatc atggagtaca ttcataagat 4140  
 agaggtgac cttgaacact taaaggaagg tggaggaaaag ttaacaccat tctttgcaa 4200  
 aggtggtg gatcagccct cacagacaag cactcagata aaagttagag ccgcatgtcc 4260  
 tggagggtgac tgcagggtgt tggatttggga gtatcggtcg tgtctacca catcctggct 4320  
 ccagtgtgga tgcagagaga gtgtgacaga ggtatcgct gtgaaccacc tgggattagt 4380  
 caagtcccaa ggtgcccaga gtgggactag ttyttcacag tgtggcagct gcactaatct 4440  
 gttgtgagg gaatatccat tccctcactc tactctctc actatcggaa attcattttg 4500  
 attcagaata aaaaccaa gtatagagct ttgggttgta ggatatgaaa ttgtacttag 4560  
 atttaagaaa aaaaaaaaaa aa 4582

<210> 186

<211> 1461

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (364)

<220>

<221> UNSURE

<222> (369)

<220>

<221> UNSURE

<222> (1433)

<400> 186

Met Ser Pro Ile Met Thr Ser Pro His Ser Pro Gly Ala Ser Gly Asn  
 1 5 10 15

Met Glu Arg Ile Thr Ser Pro Val Leu Met Gly Glu Glu Asn Asn Val  
 20 25 30

Val His Asn Gln Lys Val Glu Ile Leu Arg Lys Met Leu Gln Lys Glu  
 35 40 45

Gln Glu Arg Leu Gln Leu Leu Gln Glu Asp Tyr Asn Arg Thr Pro Ala  
 50 55 60

Gln Arg Leu Leu Lys Glu Ile Gln Glu Ala Lys Lys His Ile Pro Gln  
 65 70 75 80

Leu Gln Glu Gln Leu Ser Lys Ala Thr Gly Ser Ala Gln Asp Gly Ala  
 85 90 95

Val Val Thr Pro Ser Arg Pro Leu Gly Asp Thr Leu Thr Val Ser Glu  
 100 105 110

Ala Glu Thr Asp Pro Gly Asp Val Leu Gly Arg Thr Asp Cys Ser Ser

115	120	125
Gly Asp Ala Ser Arg Pro Ser Ser Asp Asn Ala Asp Ser Pro Lys Ser		
130	135	140
Gly Pro Lys Glu Arg Ile Tyr Leu Glu Glu Asn Pro Glu Lys Ser Glu		
145	150	155 160
Thr Ile Gln Asp Thr Asp Thr Gln Ser Leu Val Gly Ser Pro Ser Thr		
	165	170 175
Arg Ile Ala Pro His Ile Ile Gly Ala Glu Asp Asp Asp Phe Gly Thr		
	180	185 190
Glu His Glu Gln Ile Asn Gly Gln Cys Ser Cys Phe Gln Ser Ile Glu		
	195	200 205
Leu Leu Lys Ser Arg Pro Ala His Leu Ala Val Phe Leu His His Val		
	210	215 220
Val Ser Gln Phe Asp Pro Ala Thr Leu Leu Cys Tyr Leu Tyr Ser Asp		
	225	230 235 240
Leu Tyr Lys His Thr Asn Ser Lys Glu Thr Arg Arg Ile Phe Leu Glu		
	245	250 255
Phe His Gln Phe Phe Leu Asn Arg Ser Ala His Leu Lys Val Ser Val		
	260	265 270
Pro Asp Glu Met Ser Ala Asp Leu Glu Lys Arg Arg Pro Glu Leu Ile		
	275	280 285
Pro Glu Asp Leu His Arg His Tyr Ile Gln Thr Met Gln Glu Arg Val		
	290	295 300
His Pro Glu Val Gln Arg His Leu Lys Asp Phe Arg Gln Lys Arg Ser		
	305	310 315 320
Met Gly Leu Thr Leu Ala Glu Ser Glu Leu Thr Lys Leu Asp Ala Glu		
	325	330 335
Arg Asp Lys Asp Arg Leu Thr Leu Glu Lys Glu Arg Thr Cys Ala Glu		
	340	345 350
Gln Ile Val Ala Lys Ile Glu Glu Val Leu Met Xaa Ala Gln Ala Val		
	355	360 365
Xaa Glu Asp Lys Ser Ser Thr Met Gln Tyr Val Ile Leu Met Tyr Met		
	370	375 380
Lys His Leu Gly Val Lys Val Lys Glu Pro Arg Asn Leu Glu His Lys		
	385	390 395 400
Arg Gly Arg Ile Gly Phe Leu Pro Lys Ile Lys Gln Ser Met Lys Lys		
	405	410 415
Asp Lys Glu Gly Glu Glu Lys Gly Lys Arg Arg Gly Phe Pro Ser Ile		
	420	425 430
Leu Gly Pro Pro Arg Arg Pro Ser Arg His Asp Asn Ser Ala Ile Gly		

435                      440                      445  
 Arg Ala Met Glu Leu Gln Lys Ala Arg His Pro Lys His Leu Ser Thr  
 450                      455                      460  
 Pro Ser Ser Val Ser Pro Glu Pro Gln Asp Ser Ala Lys Leu Arg Gln  
 465                      470                      475                      480  
 Ser Gly Leu Ala Asn Glu Gly Thr Asp Ala Gly Tyr Leu Pro Ala Asn  
 485                      490                      495  
 Ser Met Ser Ser Val Ala Ser Gly Ala Ser Phe Ser Gln Glu Gly Gly  
 500                      505                      510  
 Lys Glu Asn Asp Thr Gly Ser Lys Gln Val Gly Glu Thr Ser Ala Pro  
 515                      520                      525  
 Gly Asp Thr Leu Asp Gly Thr Pro Arg Thr Leu Asn Thr Val Phe Asp  
 530                      535                      540  
 Phe Pro Pro Pro Pro Leu Asp Gln Val Gln Glu Glu Glu Cys Glu Val  
 545                      550                      555                      560  
 Glu Arg Val Thr Glu His Gly Thr Pro Lys Pro Phe Arg Lys Phe Asp  
 565                      570                      575  
 Ser Val Ala Phe Gly Glu Ser Gln Ser Glu Asp Glu Gln Phe Glu Asn  
 580                      585                      590  
 Asp Leu Glu Thr Asp Pro Pro Asn Trp Gln Gln Leu Val Ser Arg Glu  
 595                      600                      605  
 Val Leu Leu Gly Leu Lys Pro Cys Glu Ile Lys Arg Gln Glu Val Ile  
 610                      615                      620  
 Asn Glu Leu Phe Tyr Thr Glu Arg Ala His Val Arg Thr Leu Lys Val  
 625                      630                      635                      640  
 Leu Asp Gln Val Phe Tyr Gln Arg Val Ser Arg Glu Gly Ile Leu Ser  
 645                      650                      655  
 Pro Ser Glu Leu Arg Lys Ile Phe Ser Asn Leu Glu Asp Ile Leu Gln  
 660                      665                      670  
 Leu His Ile Gly Leu Asn Glu Gln Met Lys Ala Val Arg Lys Arg Asn  
 675                      680                      685  
 Glu Thr Ser Val Ile Asp Gln Ile Gly Glu Asp Leu Leu Thr Trp Phe  
 690                      695                      700  
 Ser Gly Pro Gly Glu Glu Lys Leu Lys His Ala Ala Ala Thr Phe Cys  
 705                      710                      715                      720  
 Ser Asn Gln Pro Phe Ala Leu Glu Met Ile Lys Ser Arg Gln Lys Lys  
 725                      730                      735  
 Asp Ser Arg Phe Gln Thr Phe Val Cln Asp Ala Glu Ser Asn Pro Leu  
 740                      745                      750  
 Cys Arg Arg Leu Gln Leu Lys Asp Ile Ile Pro Thr Gln Met Gln Arg

755	760	765
Leu Thr Lys Tyr Pro Leu Leu Leu Asp Asn Ile Ala Lys Tyr Thr Glu 770	775	780
Trp Pro Thr Glu Arg Glu Lys Val Lys Lys Ala Ala Asp His Cys Arg 785	790	795 800
Gln Ile Leu Asn Tyr Val Asn Gln Ala Val Lys Glu Ala Glu Asn Lys 805	810	815
Gln Arg Leu Glu Asp Tyr Gln Arg Arg Leu Asp Thr Ser Ser Leu Lys 820	825	830
Leu Ser Glu Tyr Pro Asn Val Glu Glu Leu Arg Asn Leu Asp Leu Thr 835	840	845
Lys Arg Lys Met Ile His Glu Gly Pro Leu Val Trp Lys Val Asn Arg 850	855	860
Asp Lys Thr Ile Asp Leu Tyr Thr Leu Leu Leu Glu Asp Ile Leu Val 865	870	875 880
Leu Leu Gln Lys Gln Asp Asp Arg Leu Val Leu Arg Cys His Ser Lys 885	890	895
Ile Leu Ala Ser Thr Ala Asp Ser Lys His Thr Phe Ser Pro Val Ile 900	905	910
Lys Leu Ser Thr Val Leu Val Arg Gln Val Ala Thr Asp Asn Lys Ala 915	920	925
Leu Phe Val Ile Ser Met Ser Asp Asn Gly Ala Gln Ile Tyr Glu Leu 930	935	940
Val Ala Gln Thr Val Ser Glu Lys Thr Val Trp Gln Asp Leu Ile Cys 945	950	955 960
Arg Met Ala Ala Ser Val Lys Glu Gln Ser Thr Lys Pro Ile Pro Leu 965	970	975
Pro Gln Ser Thr Pro Gly Glu Gly Asp Asn Asp Glu Glu Asp Pro Ser 980	985	990
Lys Leu Lys Glu Glu Gln His Gly Ile Ser Val Thr Gly Leu Gln Ser 995	1000	1005
Pro Asp Arg Asp Leu Gly Leu Glu Ser Thr Leu Ile Ser Ser Lys Pro 1010	1015	1020
Gln Ser His Ser Leu Ser Thr Ser Gly Lys Ser Glu Val Arg Asp Leu 1025	1030	1035 1040
Phe Val Ala Glu Arg Gln Phe Ala Lys Glu Gln His Thr Asp Gly Thr 1045	1050	1055
Leu Lys Glu Val Gly Glu Asp Tyr Gln Ile Ala Ile Pro Asp Ser His 1060	1065	1070
Leu Pro Val Ser Glu Glu Arg Trp Ala Leu Asp Ala Leu Arg Asn Leu		

1075	1080	1085
Gly Leu Leu Lys Gln Leu Leu Val Gln Gln Leu Gly Leu Thr Glu Lys 1090	1095	1100
Ser Val Gln Glu Asp Trp Gln His Phe Pro Arg Tyr Arg Thr Ala Ser 1105	1110	1115 1120
Gln Gly Pro Gln Thr Asp Ser Val Ile Gln Asn Ser Glu Asn Ile Lys 1125	1130	1135
Ala Tyr His Ser Gly Glu Gly His Met Pro Phe Arg Thr Gly Thr Gly 1140	1145	1150
Asp Ile Ala Thr Cys Tyr Ser Pro Arg Thr Ser Thr Glu Ser Phe Ala 1155	1160	1165
Pro Arg Asp Ser Val Gly Leu Ala Pro Gln Asp Ser Gln Ala Ser Asn 1170	1175	1180
Ile Leu Val Met Asp His Met Ile Met Thr Pro Glu Met Pro Thr Met 1185	1190	1195 1200
Glu Pro Glu Gly Gly Leu Asp Asp Ser Gly Glu His Phe Phe Asp Ala 1205	1210	1215
Arg Glu Ala His Ser Asp Glu Asn Pro Ser Glu Gly Asp Gly Ala Val 1220	1225	1230
Asn Lys Glu Glu Lys Asp Val Asn Leu Arg Ile Ser Gly Asn Tyr Leu 1235	1240	1245
Ile Leu Asp Gly Tyr Asp Pro Val Gln Glu Ser Ser Thr Asp Glu Glu 1250	1255	1260
Val Ala Ser Ser Leu Thr Leu Gln Pro Met Thr Gly Ile Pro Ala Val 1265	1270	1275 1280
Glu Ser Thr His Gln Gln Gln His Ser Pro Gln Asn Thr His Ser Asp 1285	1290	1295
Gly Ala Ile Ser Pro Phe Thr Pro Glu Phe Leu Val Gln Gln Arg Trp 1300	1305	1310
Gly Ala Met Glu Tyr Ser Cys Phe Glu Ile Gln Ser Pro Ser Ser Cys 1315	1320	1325
Ala Asp Ser Gln Ser Gln Ile Met Glu Tyr Ile His Lys Ile Glu Ala 1330	1335	1340
Asp Leu Glu His Leu Lys Glu Gly Gly Gly Lys Leu Thr Pro Phe Phe 1345	1350	1355 1360
Ala Lys Gly Trp Leu Asp Gln Pro Ser Gln Thr Ser Thr Gln Ile Lys 1365	1370	1375
Val Arg Ala Ala Cys Pro Gly Gly Asp Cys Arg Leu Leu Asp Leu Glu 1380	1385	1390
Tyr Arg Pro Cys Leu Thr Thr Ser Trp Leu Gln Cys Gly Cys Arg Glu		

1395

1400

1405

Ser Val Thr Glu Asp Leu Pro Val Asn His Leu Gly Leu Val Lys Ser  
 1410 1415 1420

Gln Gly Ala Gln Ser Gly Thr Ser Xaa Ser Gln Cys Gly Ser Cys Thr  
 1425 1430 1435 1440

Asn Leu Phe Val Arg Glu Tyr Pro Phe Pro His Ser Thr Leu Leu Thr  
 1445 1450 1455

Ile Gly Asn Ser Phe  
 1460

&lt;210&gt; 187

&lt;211&gt; 2837

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 187

tcttttgaca gatataattg ctgcttatca aagattctgt tctcgacccc caaaaggatt 60  
 tgaataatc tttcctaattg gaaaaaatgg aaaaaaagct agtgaacctt aagaagttat 120  
 gggagagaaa aaagaatcaa agccagctgc taccacacgc tcttctggag gaggaggtgg 180  
 tggcggtgga aaacgaggtg gcaagaaaga tgattctcac tgggtgtcca ggtttcagaa 240  
 gggtagacatt ccattgggacg acaaggattt caggatgttc ttctctctgga ctgctctgtt 300  
 ctgggggtgga gtcattgtttt acttgctgct caagagatcc gggagagaaa tcacttggaa 360  
 ggactttgtc aataactatc ttcaaaaagg agtagtagac agattggaag tcgtcaacaa 420  
 gcgttttgtt cgagtgcctt ttaccaccag aaaaactcct gttgatgggc aatacgtttg 480  
 gtttaataat ggcagtgttg acacctttga acggaatctg gaaactttac agcaggaatt 540  
 gggcatagaa ggagaaaatc ggggtgcctgt tgtctacatt gctgaaagtg atggctcttt 600  
 tctgctgagc atgctgccta cggtgctcat catcgccctc ttgctctaca ccattcagaag 660  
 agggcctgct ggcattggcc ggacaggccg agggatgggc ggactcttca gtgtcggaga 720  
 aaccactgcc aaggtcttaa aggatgaaat tgatgtgaag ttcaaaagatg tggctggctg 780  
 tgaggaggcc aagctagaga tcatggaatt tgtgaatttc ttgaaaaacc caaagcagta 840  
 tcaagacctt ggagcaataa tcccaaaagg tgccattctc actggctctc caggcactgg 900  
 gaagacgctg ctagtcaagg ccacagccgg agaagccaat gtcccttca tcaccgttag 960  
 tggatctgag tttttggaga tgttcgttgg tgtgggcccc gctagagtcg gagacttatt 1020  
 tgccttctgct cggaagaatg ccccttgcat cctcttcac gatgaaatcg atgcgggtgg 1080  
 aaggaagaga ggaagaggca actttggagg gcagagttag caggagaaca cactcaacca 1140  
 gctgctggtg gagatggatg gttttaatac aacaacaaat gtcgtcattt tggccggcac 1200  
 caatcgacca ggaccaccag acataaaagg aagagcttct attttcaaag ttcatctccg 1260  
 accgctaaaa ctggacagta ccctggagaa ggataaattg gcaagaaaac tggcatcttt 1320  
 aactccaggg ttttcaggtg ctgatgttgc taatgtctgt aatgaagctg cgttgattgc 1380  
 tgcaaggcat ctgtcagatt ccataaatca gaaacacttt gaacaggcaa ttgagcagat 1440  
 gatttgggtg ttaaagaaaa aaacgcaggt tctgcagcct gaggagaaaa agactgtggc 1500  
 ataccacgaa gcaggccatg cgggttgcgg ctggtatctg gagcacgcag acccgctttt 1560  
 aaaggtatcc atcatccac gtggcaaagg actaggttat gctcagtatt taccaaaaga 1620  
 acaatacttc tataccaaag agcagctctt ggataggatg tgtagtactt taggtggtcg 1680  
 agtctctgaa gaaatcttct ttggaagaat tacaactggt gctcaagatg acttgagaaa 1740  
 agtaactcag agtgcatatg cccaaattgt tcagtttggc atgaatgaaa aggttgggca 1800  
 aatctccttt gacctccac gtccagggga catggtattg gagaacactt acagtgaagc 1860  
 cactgcaaga ttgatagatg atgaagtacg aatacttatt aatgatgctt ataaaagaac 1920  
 agtagctctt ctacagaaa agaaagctga cgtggagaag gttgctcttc tgttgttaga 1980  
 aaaagaagta ttagataaga atgatattgt tgaacttttg ggccccagac catttgcgga 2040  
 aaaatctacc tatgaagaat ttgtggaagg cactggcagc ttggatgagg acacctcact 2100  
 tccagaaggc cttaaggact ggaacaagga gcggaagagg gagaaagagg agccccggg 2160  
 tgagaaagtt gccactaga ggcccagagg gaggccatct cagctgtctc actgtggttt 2220  
 cagctggtgc attatttcag ctgtggcttt cagaagaatg ggaatgctgc gctgatttta 2280  
 gccagccact ggcccagctg aaatgatggg gaaaggagtc cttagtcttc tcagcctcag 2340

```

aggtcacagt ggggtggcagg tgactttccg gaggccttga gggaaatgca cactgtccca 2400
tagcctcatt ggggttcccag acgtgctgga aaggttgagc ccagagtggc cgaggctgga 2460
ccctgtggca ccaagtgggg tcggctgacc gtgtggcagg gattgttgca mtggawtttt 2520
ggcgtgtggg aagggatgct tttttttgt cgccttctgt ttttctcag 2580
ttcccckgkg cagatgggct gtgaaattaa attggagttt tgataagaac attttaattt 2640
gacttaatat tttaaagatt gaatccagat cacttggtgc tgttttaatg gaatggtttt 2700
ttacaggagc tgtaacatam ttaaaaaatat gaatgtatta tgtaaatatg gcttctttac 2760
ataaaaaata aaatgtcaac actgtaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aaaaaaaaaa aaaaaaa 2837

```

&lt;210&gt; 188

&lt;211&gt; 686

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

```

Met Gly Glu Lys Lys Glu Ser Lys Pro Ala Ala Thr Thr Arg Ser Ser
  1              5              10              15

```

```

Gly Gly Gly Gly Gly Gly Gly Gly Lys Arg Gly Gly Lys Lys Asp Asp
      20              25              30

```

```

Ser His Trp Trp Ser Arg Phe Gln Lys Gly Asp Ile Pro Trp Asp Asp
      35              40              45

```

```

Lys Asp Phe Arg Met Phe Phe Leu Trp Thr Ala Leu Phe Trp Gly Gly
      50              55              60

```

```

Val Met Phe Tyr Leu Leu Leu Lys Arg Ser Gly Arg Glu Ile Thr Trp
      65              70              75              80

```

```

Lys Asp Phe Val Asn Asn Tyr Leu Ser Lys Gly Val Val Asp Arg Leu
      85              90              95

```

```

Glu Val Val Asn Lys Arg Phe Val Arg Val Thr Phe Thr Pro Gly Lys
      100              105              110

```

```

Thr Pro Val Asp Gly Gln Tyr Val Trp Phe Asn Ile Gly Ser Val Asp
      115              120              125

```

```

Thr Phe Glu Arg Asn Leu Glu Thr Leu Gln Gln Glu Leu Gly Ile Glu
      130              135              140

```

```

Gly Glu Asn Arg Val Pro Val Val Tyr Ile Ala Glu Ser Asp Gly Ser
      145              150              155              160

```

```

Phe Leu Leu Ser Met Leu Pro Thr Val Leu Ile Ile Ala Phe Leu Leu
      165              170              175

```

```

Tyr Thr Ile Arg Arg Gly Pro Ala Gly Ile Gly Arg Thr Gly Arg Gly
      180              185              190

```

```

Met Gly Gly Leu Phe Ser Val Gly Glu Thr Thr Ala Lys Val Leu Lys
      195              200              205

```

```

Asp Glu Ile Asp Val Lys Phe Lys Asp Val Ala Gly Cys Glu Glu Ala
      210              215              220

```

```

Lys Leu Glu Ile Met Glu Phe Val Asn Phe Leu Lys Asn Pro Lys Gln
      225              230              235              240

```



Tyr Gln Asp Leu Gly Ala Ile Ile Pro Lys Gly Ala Ile Leu Thr Gly  
 245 250 255  
 Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Thr Ala Gly Glu  
 260 265 270  
 Ala Asn Val Pro Phe Ile Thr Val Ser Gly Ser Glu Phe Leu Glu Met  
 275 280 285  
 Phe Val Gly Val Gly Pro Ala Arg Val Arg Asp Leu Phe Ala Leu Ala  
 290 295 300  
 Arg Lys Asn Ala Pro Cys Ile Leu Phe Ile Asp Glu Ile Asp Ala Val  
 305 310 315 320  
 Gly Arg Lys Arg Gly Arg Gly Asn Phe Gly Gly Gln Ser Glu Gln Glu  
 325 330 335  
 Asn Thr Leu Asn Gln Leu Leu Val Glu Met Asp Gly Phe Asn Thr Thr  
 340 345 350  
 Thr Asn Val Val Ile Leu Ala Gly Thr Asn Arg Pro Gly Pro Pro Asp  
 355 360 365  
 Ile Lys Gly Arg Ala Ser Ile Phe Lys Val His Leu Arg Pro Leu Lys  
 370 375 380  
 Leu Asp Ser Thr Leu Glu Lys Asp Lys Leu Ala Arg Lys Leu Ala Ser  
 385 390 395 400  
 Leu Thr Pro Gly Phe Ser Gly Ala Asp Val Ala Asn Val Cys Asn Glu  
 405 410 415  
 Ala Ala Leu Ile Ala Ala Arg His Leu Ser Asp Ser Ile Asn Gln Lys  
 420 425 430  
 His Phe Glu Gln Ala Ile Glu Arg Val Ile Gly Gly Leu Lys Lys Lys  
 435 440 445  
 Thr Gln Val Leu Gln Pro Glu Glu Lys Lys Thr Val Ala Tyr His Glu  
 450 455 460  
 Ala Gly His Ala Val Ala Gly Trp Tyr Leu Glu His Ala Asp Pro Leu  
 465 470 475 480  
 Leu Lys Val Ser Ile Ile Pro Arg Gly Lys Gly Leu Gly Tyr Ala Gln  
 485 490 495  
 Tyr Leu Pro Lys Glu Gln Tyr Leu Tyr Thr Lys Glu Gln Leu Leu Asp  
 500 505 510  
 Arg Met Cys Met Thr Leu Gly Gly Arg Val Ser Glu Glu Ile Phe Phe  
 515 520 525  
 Gly Arg Ile Thr Thr Gly Ala Gln Asp Asp Leu Arg Lys Val Thr Gln  
 530 535 540  
 Ser Ala Tyr Ala Gln Ile Val Gln Phe Gly Met Asn Glu Lys Val Gly  
 545 550 555 560

Gln Ile Ser Phe Asp Leu Pro Arg Gln Gly Asp Met Val Leu Glu Lys  
565 570 575

Pro Tyr Ser Glu Ala Thr Ala Arg Leu Ile Asp Asp Glu Val Arg Ile  
580 585 590

Leu Ile Asn Asp Ala Tyr Lys Arg Thr Val Ala Leu Leu Thr Glu Lys  
595 600 605

Lys Ala Asp Val Glu Lys Val Ala Leu Leu Leu Glu Lys Glu Val  
610 615 620

Leu Asp Lys Asn Asp Met Val Glu Leu Leu Gly Pro Arg Pro Phe Ala  
625 630 635 640

Glu Lys Ser Thr Tyr Glu Glu Phe Val Glu Gly Thr Gly Ser Leu Asp  
645 650 655

Glu Asp Thr Ser Leu Pro Glu Gly Leu Lys Asp Trp Asn Lys Glu Arg  
660 665 670

Glu Lys Glu Lys Glu Glu Pro Pro Gly Glu Lys Val Ala Asn  
675 680 685

<210> 189

<211> 627

<212> DNA

<213> Homo sapiens

<400> 189

gattggagtt cttttcttaa atatccaaat aagattatag ctatgttttt accaaatgtt 60  
tgtgcggttaa atagagagtg gatggaaatt aaccctagaa aggatagttg taacttttaa 120  
aaagtgtgatt aactatttcg tgtgctaatt tgagtttttc tgaatactcc aatattgttt 180  
cctttaacac ctgtcttcag tttacaatca cctaacttcc cagcggttgg gtctttttct 240  
ctgtctgacc ctgtcttatt tctcctacaa agacatatcc tgcgctgtac ttcagatact 300  
tttttcgagg aacatttttg atttgtggca taaagtaact gtctaaagga aatcttctga 360  
gaggatctgg tcatttttatg aaagggggcaa ttaaggggaa atggaagcag atctttttaa 420  
gaaggagcat ttgaaattag cccaggaatc atgtccggcg agtcctgtct ttttgtacct 480  
gggcataata gtcagccaca cagagctaga gttagttcaa gaattgtctt tcttgatcgt 540  
gctatatatt tggaacacg ttagatacag aggtaagatg tcaaaattct gaaatacaca 600  
caatatagga tcaaaaaaaaa aaaaaaa 627

<210> 190

<211> 63

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Ala Asp Leu Leu Lys Lys Glu His Leu Lys Leu Ala Gln Glu  
1 5 10 15

Ser Cys Pro Ala Ser Pro Ala Leu Leu Tyr Leu Gly Ile Ile Val Ser  
20 25 30

His Thr Glu Leu Glu Leu Val Gln Glu Leu Ser Phe Leu Ile Val Leu  
35 40 45

Tyr Phe Trp Lys His Val Arg Tyr Arg Gly Lys Met Ser Lys Phe

50

55

60

<210> 191  
 <211> 868  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (733)

<400> 191  
 attctgtccc tgccttaga aaacctaaaa taccaagggt gtcattgctgg caactccctg 60  
 cccagtcctg cacaagcct tggctgtgtg tggcaccctc tgcctcctac cccagagcag 120  
 ctggctccat tggcttctcc ctgcaccagc cctgtcctca ggggtcagga aaaagcacac 180  
 agctttcttt cctctcctcc agaggcctgg aaggagggtg gaggtccagt aagggcctgg 240  
 ctgccttgga tttcttggtc' ctgccttgcc aactgcaccc tgtagctcct gctccctgtg 300  
 accccagaac agagggtgctg ccttccctgt ctccctagaca aagcacaaag ggatgccctg 360  
 cttggcttga gcctgcccac ctgaaggatt ttctctgccc cagggacctt ccatccctga 420  
 atacaaggct ctaggcaact tctctctggg tggtagacac tagaatgcct ggcattagcc 480  
 ctgaaagga ggttggggtg tatgggtagt gagctagggt gggagaaagg tgggtctgaa 540  
 aggacagatg ctagtgttag tttcactcac tcattcattc attagtgcaa cagtactgag 600  
 caccacctgc actagaggca gagggtgtaa caagataccc ttttgcttgg ggggacgtcc 660  
 acttccccatg ggtttggcta tttccaggaa agccctcag tctcctccc tgttctggct 720  
 gtgtgtgaag gangtgtgtg agcaggccca atcctttgca gcaagaatga gaggtcagag 780  
 tattccattg cacacgcacc ctggggctga cagactgtg ccccttagcc ttcattgcatg 840  
 cccaagcact ggcagctttg cagccctc 868

<210> 192  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (62)

<400> 192  
 Met Leu Val Val Val Ser Leu Thr His Ser Phe Ile Ser Ala Thr Val  
 1 5 10 15  
 Leu Ser Thr Thr Cys Thr Arg Gly Arg Gly Val Asn Lys Ile Pro Phe  
 20 25 30  
 Cys Leu Gly Gly Arg Pro Leu Pro Met Gly Leu Ala Ile Ser Arg Lys  
 35 40 45  
 Ala Pro Gln Ser Ser Ser Leu Phe Trp Leu Cys Val Lys Xaa Val Cys  
 50 55 60  
 Glu Gln Ala Gln Ser Phe Ala Ala Arg Met Arg Gly Gln Ser Ile Pro  
 65 70 75 80  
 Leu His Thr His Pro Gly Ala Asp Arg Leu Val Pro Pro Ser Leu His  
 85 90 95  
 Ala Cys Pro Ser Thr Gly Ser Phe Ala Ala Pro  
 100 105

<210> 193  
 <211> 467  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (57)

<220>  
 <221> unsure  
 <222> (254)

<400> 193  
 tggctatccc tagaagcact tcattccatct taaccacccc aaacgggac ccttcanatc 60  
 tcataccagc taagatgcaa gaaaggaata tttgagagca agcagccctg tccaggggc 120  
 cccaggtatg tgtagaggcc cagtgggggt ggccacttgg tgtttctacc acccctgcc 180  
 atccagtctg gccaggtacc tacctgggag gttgggtgtac ttggcctaag tacttcatgc 240  
 tttattcagg ctgnttcccc acagcaccgg caggaaatga aggtgcactt atatgcattc 300  
 ctgcagggaat aaagagtggg tggcctgccc agcccagcac cacagccttt ccccagccag 360  
 gagagaccac ctaaggatca aggcagctcc tgttttcttg gttctgtgac actcgagtct 420  
 gagccagccc ctcaggaatt gcctcaaaaag agaaaaaaaa aaaaaaa 467

<210> 194  
 <211> 1035  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 aatctttttg ttgtcaagct tgagggtgtg caggcttgag atctggccat acacttgagt 60  
 gacaatgaca tccactttgc cttctctctc acaggtgtcc actcccaggt ccaactgcag 120  
 acttcgaatt cggccttcat ggcctagatg attgcaagtc aatggaagga gctgcagagg 180  
 caaatcaaac ggcagcacag ctggattctc agggctcttg ataccatcaa agccgagata 240  
 ctggctactg atgtgtctgt ggaggatgag gaagggactg gaagccccc aagctgaggtt 300  
 caactatgct acctggaagc acaaagagat gctgttgagc agatgtccct caagctgttc 360  
 agcagcagct ataccagcag cagcaagcga aaggaagagt ttgctgatat gtcaaaagt 420  
 tcattcagtg ggaagcaatg ggcttctgga ctttgattca gaatatcmgg agctctggga 480  
 ttggctgatt gacatggagt cccttgtgat ggacagccac gacctgatga tgcagagga 540  
 gcagcagcag catctttaca agcgatacag tgtggaaatg tccatcagac acctgaaaaa 600  
 gacggagctg cttagtaagg ttgaagcttt gaagaaaggt ggcgttttac taccaaatga 660  
 tctccttgaa aaagtggatt caattaatga aaaatgggaa ctrcttgggg tatttgcat 720  
 tttattactg tttgtagggt atgtgtacat tttttgcgta gtgaagtact ctgtccgatt 780  
 tctaatttga ggcacaaata tctctctctt tcaattcact acctacgttt caaacaagct 840  
 attcatgcta ttatgggaaa gacactgctt tccctctctt gttgattttt ttttttctg 900  
 agcttgtccc ctctcagatt ttaataattt tgggtcttta atacatgaaa aagtaagtaa 960  
 aatatgccat gtattatggg tatgcaccaa gtcaactata atacagtata tctgatatat 1020  
 aaaaaaaaaa aaaaa 1035

<210> 195  
 <211> 179  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (37)

<220>  
 <221> UNSURE

&lt;222&gt; (73)

&lt;400&gt; 195

Met Cys Leu Trp Arg Met Arg Lys Gly Leu Glu Ala Pro Arg Leu Arg  
 1 5 10 15

Phe Asn Tyr Ala Thr Trp Lys His Lys Glu Met Leu Leu Ser Arg Cys  
 20 25 30

Pro Ser Ser Cys Xaa Ala Ser Ser Ile Pro Ala Ala Ala Ser Glu Arg  
 35 40 45

Lys Ser Leu Leu Ile Cys Gln Lys Phe His Ser Val Gly Ser Asn Gly  
 50 55 60

Leu Leu Asp Phe Asp Ser Glu Tyr Xaa Glu Leu Trp Asp Trp Leu Ile  
 65 70 75 80

Asp Met Glu Ser Leu Val Met Asp Ser His Asp Leu Met Met Ser Glu  
 85 90 95

Glu Gln Gln Gln His Leu Tyr Lys Arg Tyr Ser Val Glu Met Ser Ile  
 100 105 110

Arg His Leu Lys Lys Thr Glu Leu Leu Ser Lys Val Glu Ala Leu Lys  
 115 120 125

Lys Gly Gly Val Leu Leu Pro Asn Asp Leu Leu Glu Lys Val Asp Ser  
 130 135 140

Ile Asn Glu Lys Trp Glu Leu Leu Gly Val Phe Ala Phe Leu Leu Leu  
 145 150 155 160

Phe Val Gly Tyr Val Tyr Ile Phe Cys Val Val Lys Tyr Ser Val Arg  
 165 170 175

Phe Leu Ile

&lt;210&gt; 196

&lt;211&gt; 3831

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 196

gcagcaggtc aaacaaggca tctcctagta ttgcatccta cagatgtgct gtaaacaatca 60  
 aaagaagacg gtgggatcag gagatgctgt tttggaaaga agtgagggtt agacttctcc 120  
 atgttaacca tgagcgtgac actttccccc ctgagggtcac aggacctgga tcccatggct 180  
 actgatgctt caccatggc catcaacatg acacccactg tggagcaggg tgagggagaa 240  
 gaggcaatga aggacatgga ctctgaccag cagtatgaaa agccaccccc actacacaca 300  
 ggggctgact ggaagattgt cctccactta cctgaaattg agacctggct cgggatgacc 360  
 tcagagaggg tccgagacct aacctattca gtccagcagg attcggacag caagcatgtg 420  
 gatgtacatc tagttcaact aaaggacatt tgtgaagata tttctgatca tgttgagcaa 480  
 atccatgccc tccctgaaac agagtctctc cttaaagctgc tgtcttactc tgtcaacgtg 540  
 atagtggaca tccacgcagt gcagctctc tggcaccagc ttcgagtctc agtgcctggt 600  
 ctgcgggagc gcattctgca aggtctgcag gacgccaatg gcaactacac taggcagacg 660  
 gacattctgc aagctttctc tgaagagaca aaagagggcc ggcttgattc tctaacagaa 720  
 gtggatgact caggacaatt aaccatcaaa tgttctcaaa attacttgct tctggattgt 780  
 ggcattactg cattcgaact gtctgactac agtccaagtg aggatttgct cagtgggcta 840

```

gggtgacatga cctctagcca agtcaaaacc aaaccctttg actcttggag ctacagttag 900
atggaaaagg agtttcttga gcttatccga agtggtgggt tacttacggt agctgctgac 960
tctatctcta ccaatggcag tgaagcagtt actgaggagg tatctcaagt atctctctca 1020
gtagacgaca aagggtggatg tgaggaagac aatgttcttg cagtcgaaga gcaaccaggc 1080
ttaacactgg ggggtgtcatc atcttcagga gaagctctga caaatgctgc tcaaccctcc 1140
tctgagactg tgcagcaaga atccagttcc tcttcccatc atgatgcaaa gaatcagcag 1200
cctgttccct gtgaaaatgc aacccccaaa cgaaccatca gagattgctt taattataac 1260
gaggactctc ccacacagcc tacattgcca aaaagaggac tttttcttaa agaggaaact 1320
tttaagaatg atctgaaagg caatgggtgga aagaggcaaa tgggtgatct aaagcctgag 1380
atgagcagaa gcaccccttc gctagtagat cctctgaca gatccaaact ttgcctggta 1440
ttgagctctt ctaccccaa cagcccttct gctgccagcc agtcttatga gtgtttacac 1500
aagggtggga atgggaacct tgaaaacaca gtcaaatctt acattaaaga aatttcttcc 1560
agcctgggaa ggtttaacga ctgtataaaa gagaatcttc gacttaaaaa gccacacaag 1620
acctcagaag aggtgcctcc atgccgaaca cctaaacggg ggactgggtt aggcaaaaca 1680
gctaaaaata caaagagctc agcagtgcc aatggagagc tttcttatac ttccaaggcc 1740
atagaggggc cacaacaaaa ttctgcttcc acatcctcac ttgagccttg taatcagaga 1800
agttggaatg ccaaatgcca attgcagtca gaaacatcca gttcaccagc ttttactcag 1860
agcagtgaat cctctgttgg ctcagacaac atcatgtctc cggtgccact tctttcaaaa 1920
cacaaaagca aaaaaggcca agcctcctct ccaagtcacg tcactaggaa tggtgagggt 1980
gtggaggcct ggtatggctc tgatgaatac cttagcactgc cctctcacct taagcagaca 2040
gaagtattgg ctttgaagtt ggaaaacctt acaaagcttc tgctcagaa acccagagga 2100
gaaaccatcc agaattatga tgactgggaa ctgtctgaaa tgaattcaga ttctgaaatc 2160
tatccaacct atcatgtcaa aaagaagcat acaaggctag gcagggtgtc tccaagctca 2220
tctagtga caagcctctc actaggggag agcattgaat ctgggccccct gagtgcatt 2280
cttcttgatg aggagtcag tatgcctctc gctggcatga aaaagtatgc tgatgagaag 2340
tcagaaaagag cttcatcctc tgagaaaaat gagagccatt ctgccactaa atcagcttta 2400
attcagaaac tgatgcaaga tattcagcac caagacaact atgaagccat atgggaaaaa 2460
atagaggggt ttgtaacaa actggatgaa ttcattcaat ggtaaatga agccatggaa 2520
actacagaga attggactcc ccctaaagca gagatggatg acctaaact gtatctggag 2580
acacacttga gttttaagtt gaatgtagac agtcattgtg ctctcaagga agctgtggag 2640
gaggaaggag accaacttct tgagcttatt gcattctaca aagcaggact gaaggacatg 2700
ctgcggatga ttgcaagtca atggaaggag ctgcagaggc aaatcaaacg gcagcacagc 2760
tggattctca gggctctgga taccatcaaa gccgagatac tggctactga tgtgtctgtg 2820
gaggatgagg aagggactgg aagccccaag gctgagggtc aactatgcta cctggaagca 2880
caaagagatg ctgttgagca gatgtccctc aagctgtaca gcgagcagta taccagcagc 2940
agcaagcgaa aggaagagtt tgctgatatg tcaaaagttc attcagtggg aagcaatggg 3000
cttctggact ttgattcaga atatcaggag ctctgggatt ggctgattga catggagtcc 3060
cttctgtatg acagccacga cctgatgatg tcagaggagc agcagcagca tctttacaag 3120
cgatacagtg tggaaatgtc catcagacac ctgaaaaaga cggagctgct tagtaagggt 3180
gaagctttga agaaagggtg cgttttacta ccaaatgac tccttgaaaa agtggattca 3240
attaatgaaa aatgggaact gcttggggta tttgcatttt tattactgtt tgtaggttat 3300
gtgtacattt tttgcgtagt gaagtactct gtccgatttc taatttgagg cacaaatatt 3360
tctctcttcc aattcactac ctacgtttca aacaagctat tcatgctatt atgggaaaga 3420
cactgctttt cctcttctgt tgattttttt tttttctgag ctgtccctc ctcagatttt 3480
aataattttg gttctttaat acatgaaaaa gtaagtaaaa tatgccatgt attatgggta 3540
tgcaccaagt caactataat acagtatatc tgatatatac tgactgtcat gcttgaatga 3600
atgttaatat aatttattct gaaggtagat gtgagagaca tctactgttt aactattttac 3660
tgtaccctta agatgaaaag tggagttgtc actacagctt tcaagtcaca ctaaagccac 3720
caaaaacaaag atgcaaatgt gacccaaatc tgaattgcag aattgaatca gcctgtgttt 3780
tgtgcctcaa tttccagctc acttttaaca aaagccaaaa aaaaaaaaaa a 3831

```

&lt;210&gt; 197

&lt;211&gt; 1075

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 197

Met Leu Thr Met Ser Val Thr Leu Ser Pro Leu Arg Ser Gln Asp Leu

1

5

10

15

Asp Pro Met Ala Thr Asp Ala Ser Pro Met Ala Ile Asn Met Thr Pro  
 20 25 30  
 Thr Val Glu Gln Gly Glu Gly Glu Glu Ala Met Lys Asp Met Asp Ser  
 35 40 45  
 Asp Gln Gln Tyr Glu Lys Pro Pro Leu His Thr Gly Ala Asp Trp  
 50 55 60  
 Lys Ile Val Leu His Leu Pro Glu Ile Glu Thr Trp Leu Arg Met Thr  
 65 70 75 80  
 Ser Glu Arg Val Arg Asp Leu Thr Tyr Ser Val Gln Gln Asp Ser Asp  
 85 90 95  
 Ser Lys His Val Asp Val His Leu Val Gln Leu Lys Asp Ile Cys Glu  
 100 105 110  
 Asp Ile Ser Asp His Val Glu Gln Ile His Ala Leu Leu Glu Thr Glu  
 115 120 125  
 Phe Ser Leu Lys Leu Leu Ser Tyr Ser Val Asn Val Ile Val Asp Ile  
 130 135 140  
 His Ala Val Gln Leu Leu Trp His Gln Leu Arg Val Ser Val Leu Val  
 145 150 155 160  
 Leu Arg Glu Arg Ile Leu Gln Gly Leu Gln Asp Ala Asn Gly Asn Tyr  
 165 170 175  
 Thr Arg Gln Thr Asp Ile Leu Gln Ala Phe Ser Glu Glu Thr Lys Glu  
 180 185 190  
 Gly Arg Leu Asp Ser Leu Thr Glu Val Asp Asp Ser Gly Gln Leu Thr  
 195 200 205  
 Ile Lys Cys Ser Gln Asn Tyr Leu Ser Leu Asp Cys Gly Ile Thr Ala  
 210 215 220  
 Phe Glu Leu Ser Asp Tyr Ser Pro Ser Glu Asp Leu Leu Ser Gly Leu  
 225 230 235 240  
 Gly Asp Met Thr Ser Ser Gln Val Lys Thr Lys Pro Phe Asp Ser Trp  
 245 250 255  
 Ser Tyr Ser Glu Met Glu Lys Glu Phe Pro Glu Leu Ile Arg Ser Val  
 260 265 270  
 Gly Leu Leu Thr Val Ala Ala Asp Ser Ile Ser Thr Asn Gly Ser Glu  
 275 280 285  
 Ala Val Thr Glu Glu Val Ser Gln Val Ser Leu Ser Val Asp Asp Lys  
 290 295 300  
 Gly Gly Cys Glu Glu Asp Asn Ala Ser Ala Val Glu Glu Gln Pro Gly  
 305 310 315 320  
 Leu Thr Leu Gly Val Ser Ser Ser Ser Gly Glu Ala Leu Thr Asn Ala  
 325 330 335

Ala Gln Pro Ser Ser Glu Thr Val Gln Gln Glu Ser Ser Ser Ser Ser  
 340 345 350  
 His His Asp Ala Lys Asn Gln Gln Pro Val Pro Cys Glu Asn Ala Thr  
 355 360 365  
 Pro Lys Arg Thr Ile Arg Asp Cys Phe Asn Tyr Asn Glu Asp Ser Pro  
 370 375 380  
 Thr Gln Pro Thr Leu Pro Lys Arg Gly Leu Phe Leu Lys Glu Glu Thr  
 385 390 395 400  
 Phe Lys Asn Asp Leu Lys Gly Asn Gly Gly Lys Arg Gln Met Val Asp  
 405 410 415  
 Leu Lys Pro Glu Met Ser Arg Ser Thr Pro Ser Leu Val Asp Pro Pro  
 420 425 430  
 Asp Arg Ser Lys Leu Cys Leu Val Leu Gln Ser Ser Tyr Pro Asn Ser  
 435 440 445  
 Pro Ser Ala Ala Ser Gln Ser Tyr Glu Cys Leu His Lys Val Gly Asn  
 450 455 460  
 Gly Asn Leu Glu Asn Thr Val Lys Phe His Ile Lys Glu Ile Ser Ser  
 465 470 475 480  
 Ser Leu Gly Arg Leu Asn Asp Cys Tyr Lys Glu Lys Ser Arg Leu Lys  
 485 490 495  
 Lys Pro His Lys Thr Ser Glu Glu Val Pro Pro Cys Arg Thr Pro Lys  
 500 505 510  
 Arg Gly Thr Gly Ser Gly Lys Gln Ala Lys Asn Thr Lys Ser Ser Ala  
 515 520 525  
 Val Pro Asn Gly Glu Leu Ser Tyr Thr Ser Lys Ala Ile Glu Gly Pro  
 530 535 540  
 Gln Thr Asn Ser Ala Ser Thr Ser Ser Leu Glu Pro Cys Asn Gln Arg  
 545 550 555 560  
 Ser Trp Asn Ala Lys Leu Gln Leu Gln Ser Glu Thr Ser Ser Ser Pro  
 565 570 575  
 Ala Phe Thr Gln Ser Ser Glu Ser Ser Val Gly Ser Asp Asn Ile Met  
 580 585 590  
 Ser Pro Val Pro Leu Leu Ser Lys His Lys Ser Lys Lys Gly Gln Ala  
 595 600 605  
 Ser Ser Pro Ser His Val Thr Arg Asn Gly Glu Val Val Glu Ala Trp  
 610 615 620  
 Tyr Gly Ser Asp Glu Tyr Leu Ala Leu Pro Ser His Leu Lys Gln Thr  
 625 630 635 640  
 Glu Val Leu Ala Leu Lys Leu Glu Asn Leu Thr Lys Leu Leu Pro Gln  
 645 650 655



Lys Pro Arg Gly Glu Thr Ile Gln Asn Ile Asp Asp Trp Glu Leu Ser  
 660 665 670  
 Glu Met Asn Ser Asp Ser Glu Ile Tyr Pro Thr Tyr His Val Lys Lys  
 675 680 685  
 Lys His Thr Arg Leu Gly Arg Val Ser Pro Ser Ser Ser Asp Ile  
 690 695 700  
 Ala Ser Ser Leu Gly Glu Ser Ile Glu Ser Gly Pro Leu Ser Asp Ile  
 705 710 715 720  
 Leu Ser Asp Glu Glu Ser Ser Met Pro Leu Ala Gly Met Lys Lys Tyr  
 725 730 735  
 Ala Asp Glu Lys Ser Glu Arg Ala Ser Ser Ser Glu Lys Asn Glu Ser  
 740 745 750  
 His Ser Ala Thr Lys Ser Ala Leu Ile Gln Lys Leu Met Gln Asp Ile  
 755 760 765  
 Gln His Gln Asp Asn Tyr Glu Ala Ile Trp Glu Lys Ile Glu Gly Phe  
 770 775 780  
 Val Asn Lys Leu Asp Glu Phe Ile Gln Trp Leu Asn Glu Ala Met Glu  
 785 790 795 800  
 Thr Thr Glu Asn Trp Thr Pro Pro Lys Ala Glu Met Asp Asp Leu Lys  
 805 810 815  
 Leu Tyr Leu Glu Thr His Leu Ser Phe Lys Leu Asn Val Asp Ser His  
 820 825 830  
 Cys Ala Leu Lys Glu Ala Val Glu Glu Glu Gly His Gln Leu Leu Glu  
 835 840 845  
 Leu Ile Ala Ser His Lys Ala Gly Leu Lys Asp Met Leu Arg Met Ile  
 850 855 860  
 Ala Ser Gln Trp Lys Glu Leu Gln Arg Gln Ile Lys Arg Gln His Ser  
 865 870 875 880  
 Trp Ile Leu Arg Ala Leu Asp Thr Ile Lys Ala Glu Ile Leu Ala Thr  
 885 890 895  
 Asp Val Ser Val Glu Asp Glu Glu Gly Thr Gly Ser Pro Lys Ala Glu  
 900 905 910  
 Val Gln Leu Cys Tyr Leu Glu Ala Gln Arg Asp Ala Val Glu Gln Met  
 915 920 925  
 Ser Leu Lys Leu Tyr Ser Glu Gln Tyr Thr Ser Ser Ser Lys Arg Lys  
 930 935 940  
 Glu Glu Phe Ala Asp Met Ser Lys Val His Ser Val Gly Ser Asn Gly  
 945 950 955 960  
 Leu Leu Asp Phe Asp Ser Glu Tyr Gln Glu Leu Trp Asp Trp Leu Ile  
 965 970 975

Asp Met Glu Ser Leu Val Met Asp Ser His Asp Leu Met Met Ser Glu  
 980 985 990

Glu Gln Gln Gln His Leu Tyr Lys Arg Tyr Ser Val Glu Met Ser Ile  
 995 1000 1005

Arg His Leu Lys Lys Thr Glu Leu Leu Ser Lys Val Glu Ala Leu Lys  
 1010 1015 1020

Lys Gly Gly Val Leu Leu Pro Asn Asp Leu Leu Glu Lys Val Asp Ser  
 1025 1030 1035 1040

Ile Asn Glu Lys Trp Glu Leu Leu Gly Val Phe Ala Phe Leu Leu Leu  
 1045 1050 1055

Phe Val Gly Tyr Val Tyr Ile Phe Cys Val Val Lys Tyr Ser Val Arg  
 1060 1065 1070

Phe Leu Ile  
 1075

<210> 198  
 <211> 3113  
 <212> DNA  
 <213> Homo sapiens

<400> 198  
 gcaaacacat tgaagtacag gtagccacagg aaactagaaa tgtatctact ggctctgctg 60  
 aaaatgaaga aaagtcagaa gttcaagcaa tcatcgaatc tactcctgag ctggatatgg 120  
 acaaagatct cagtggtatat aaaggttcaa gcaactccac caaaggcata gagaacaaag 180  
 cttttgatcg caatacagaa tctctctttg aagaactgtc ttcagctggc tcaggcctaa 240  
 taggagatgt ggatgaagga gcagatttac taggaatggg tcgggaagtt gagaatctta 300  
 tattagaaaa tacacaactg ttggaaacca aaaatgcttt gaacatagtg aagaatgatt 360  
 tgatagcaaa agtggatgaa ctgacctgtg agaaagatgt gctgcaaggg gaattggagg 420  
 ctgtgaagca agccaaactg aaactagagg aaaagaacag agaattggag gaagagctta 480  
 ggaaagctcg ggcagaagct gaagatgcag ggcaaaaagc aaaagatgac gatgatagtg 540  
 atattccac agccagagg aaacggttta cttagataga aatggccctg gttctcatgg 600  
 agcgaaccca gtataaagag agattgatgg agcttcagga agctgttcga tggacagaga 660  
 tgattcgggc atcacgagaa aatccagcca tgcaggaaaa aaaaaggcca agcatttggc 720  
 agtttttcag ccgacttttc agtctctcaa gtaacacgac taagaagcct gaaccacctg 780  
 ttaatctgaa gtacaatgca cccacgtctc atgttactcc gtccgtcaag aaaagaagca 840  
 gcaccttatc tcagctccct ggggataagt ccaaagcctt tgatttccct agtgaagaaa 900  
 ctgaagctag tttagcctca cgcagagaaac aaaagagaga gcagtatcgt caggtaaaag 960  
 cacatgttca gaaggaagac ggtagagtgc aggtcttttg ctggagtctg cctcagaagt 1020  
 acaaacagggt aaccaatggg caaggtgaaa ataagatgaa aaatttacct gtgcctgtct 1080  
 atctcagacc tctggatgaa aaagatacat caatgaagct gtggtgtgct gttggagtca 1140  
 atttatctgg tgggaagacc agagatgggt gttctgttgt tggagcaagt gtattttaca 1200  
 aggatgttgc tggtttggtg acagaaggca gtaaacagcg aagtgcctct cagagtagtt 1260  
 tagataagtt agatcaggaa cttaaggaac agcagaagga gttaaaaaat caagaagaat 1320  
 tatccagctc agtttggatc tgtaccagca ctcattcggc tacaaaagtt cttattattg 1380  
 atgctgttca acctggcaac atcctagaca gtttactgt ttgcaactct catgttctgt 1440  
 gcattgcaag tgtgccaggt gcacgagaaa cagactacc tgcaggagaa gatctttcag 1500  
 aatctggtca ggtagacaaa gcattcttat gtggaagtat gacaagcaac agctcagcag 1560  
 agacagacag cctgttagga ggcacacag tggttggttg ttctgcagaa ggtgtgacgg 1620  
 gagctgccac tttccctagt acaaatgggt cttctccagt gatggataaa ccaccagaaa 1680  
 tggaaagcaga aaatagttag gttgatgaaa atgttccaac agcagaagaa gcaactgaag 1740  
 ctacagaagg gaatgcgggg tcagctgaag acacagtgga catctcccaa actggcgtct 1800  
 acacagagca tgtctttaca gatcctttgg gatttcagat cccagaagac ctctcccag 1860  
 tgtatcagtc gagcaatgac tcagatgcat ataaagatca aatatcagta ctgccaaatg 1920

```

aacaagactt ggtgagagaa gaagcccaga aaatgagtag tcttttacca actatgtggc 1980
ttggagctca aaatggctgt ttgtatgtcc attcatctgt agcccagtgg aggaaatgtc 2040
tccattccat taaacttaaa gattcgattc tcagtattgt acacgtgaag ggaatcgtgt 2100
tagtagccct ggctgacggc acccttgcaa tctttcacag aggagtggat gggcagtggg 2160
atttgcataa ctatcacctc ttagaccttg gacggcctca tcattccatc cgttgcatga 2220
ctgtggtaca tgacaaagtc tgggtgtggc ataggaacaa aatctatgtg gtgcagccaa 2280
aggccatgaa aatagagaaa tcttttgatg cacatcccag gaaggagagc caagtgcgac 2340
agcttgctgt ggtgggggat ggcgtgtggg tctccattcg cttggattct acgctccgtc 2400
tctatcatgc acacacttat caacatctac aggatgtgga cattgagcct tatgtaagca 2460
aaatgttagg tactggaaaa ctgggcttct cttttgtgag aattacagct cttatgggtg 2520
cttgaatcg tttgtgggtg gggacaggaa atggtgtcat tatctccatc ccattgacag 2580
aaagtaagta tttttttaga taactgccat ggaacaaata ggagaattat aggaaatagt 2640
tatgtctgaa attcaaactc gtgttagctc aagaaaatca gtgatggcaa agatctagct 2700
atagttaact tcaactcaat gaaacttata aattctagga aaataagttt tcatgtatca 2760
agaccaatac tcataattaa aagtttttcg ttgtcaaac attttcacag ttcaggaatc 2820
acagtccctat ttcatctttt gaaataaaaag ttaaagtcca tttttcttaa gccttattat 2880
accattatcc aaaaacacta cctagcattc atcttagttt ttcatatctc cttagcagat 2940
agtttagtat attccatttg tcttatttga ggtttaaaaa aagttgtgga agaagtttct 3000
caggagttca gcaagccttt ccatttatct tctattttta aagaatgtga tttattgttt 3060
ttatgaataa aatatacctc gtgtgtttct caaaaaaaa aaaaaaaaaa aaa 3113

```

&lt;210&gt; 199

&lt;211&gt; 828

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 199

```

Met Asp Lys Asp Leu Ser Gly Tyr Lys Gly Ser Ser Thr Pro Thr Lys
  1             5             10             15

Gly Ile Glu Asn Lys Ala Phe Asp Arg Asn Thr Glu Ser Leu Phe Glu
      20             25             30

Glu Leu Ser Ser Ala Gly Ser Gly Leu Ile Gly Asp Val Asp Glu Gly
      35             40             45

Ala Asp Leu Leu Gly Met Gly Arg Glu Val Glu Asn Leu Ile Leu Glu
      50             55             60

Asn Thr Gln Leu Leu Glu Thr Lys Asn Ala Leu Asn Ile Val Lys Asn
      65             70             75             80

Asp Leu Ile Ala Lys Val Asp Glu Leu Thr Cys Glu Lys Asp Val Leu
      85             90             95

Gln Gly Glu Leu Glu Ala Val Lys Gln Ala Lys Leu Lys Leu Glu Glu
      100            105            110

Lys Asn Arg Glu Leu Glu Glu Glu Leu Arg Lys Ala Arg Ala Glu Ala
      115            120            125

Glu Asp Ala Gly Gln Lys Ala Lys Asp Asp Asp Ser Asp Ile Pro
      130            135            140

Thr Ala Gln Arg Lys Arg Phe Thr Arg Val Glu Met Ala Arg Val Leu
      145            150            155            160

Met Glu Arg Asn Gln Tyr Lys Glu Arg Leu Met Glu Leu Gln Glu Ala
      165            170            175

```

Val Arg Trp Thr Glu Met Ile Arg Ala Ser Arg Glu Asn Pro Ala Met  
 180 185 190  
 Gln Glu Lys Lys Arg Ser Ser Ile Trp Gln Phe Phe Ser Arg Leu Phe  
 195 200 205  
 Ser Ser Ser Ser Asn Thr Thr Lys Lys Pro Glu Pro Pro Val Asn Leu  
 210 215 220  
 Lys Tyr Asn Ala Pro Thr Ser His Val Thr Pro Ser Val Lys Lys Arg  
 225 230 235 240  
 Ser Ser Thr Leu Ser Gln Leu Pro Gly Asp Lys Ser Lys Ala Phe Asp  
 245 250 255  
 Phe Leu Ser Glu Glu Thr Glu Ala Ser Leu Ala Ser Arg Arg Glu Gln  
 260 265 270  
 Lys Arg Glu Gln Tyr Arg Gln Val Lys Ala His Val Gln Lys Glu Asp  
 275 280 285  
 Gly Arg Val Gln Ala Phe Gly Trp Ser Leu Pro Gln Lys Tyr Lys Gln  
 290 295 300  
 Val Thr Asn Gly Gln Gly Glu Asn Lys Met Lys Asn Leu Pro Val Pro  
 305 310 315 320  
 Val Tyr Leu Arg Pro Leu Asp Glu Lys Asp Thr Ser Met Lys Leu Trp  
 325 330 335  
 Cys Ala Val Gly Val Asn Leu Ser Gly Gly Lys Thr Arg Asp Gly Gly  
 340 345 350  
 Ser Val Val Gly Ala Ser Val Phe Tyr Lys Asp Val Ala Gly Leu Asp  
 355 360 365  
 Thr Glu Gly Ser Lys Gln Arg Ser Ala Ser Gln Ser Ser Leu Asp Lys  
 370 375 380  
 Leu Asp Gln Glu Leu Lys Glu Gln Gln Lys Glu Leu Lys Asn Gln Glu  
 385 390 395 400  
 Glu Leu Ser Ser Leu Val Trp Ile Cys Thr Ser Thr His Ser Ala Thr  
 405 410 415  
 Lys Val Leu Ile Ile Asp Ala Val Gln Pro Gly Asn Ile Leu Asp Ser  
 420 425 430  
 Phe Thr Val Cys Asn Ser His Val Leu Cys Ile Ala Ser Val Pro Gly  
 435 440 445  
 Ala Arg Glu Thr Asp Tyr Pro Ala Gly Glu Asp Leu Ser Glu Ser Gly  
 450 455 460  
 Gln Val Asp Lys Ala Ser Leu Cys Gly Ser Met Thr Ser Asn Ser Ser  
 465 470 475 480  
 Ala Glu Thr Asp Ser Leu Leu Gly Gly Ile Thr Val Val Gly Cys Ser  
 485 490 495

Ala Glu Gly Val Thr Gly Ala Ala Thr Ser Pro Ser Thr Asn Gly Ala  
 500 505 510  
 Ser Pro Val Met Asp Lys Pro Pro Glu Met Glu Ala Glu Asn Ser Glu  
 515 520 525  
 Val Asp Glu Asn Val Pro Thr Ala Glu Glu Ala Thr Glu Ala Thr Glu  
 530 535 540  
 Gly Asn Ala Gly Ser Ala Glu Asp Thr Val Asp Ile Ser Gln Thr Gly  
 545 550 555 560  
 Val Tyr Thr Glu His Val Phe Thr Asp Pro Leu Gly Val Gln Ile Pro  
 565 570 575  
 Glu Asp Leu Ser Pro Val Tyr Gln Ser Ser Asn Asp Ser Asp Ala Tyr  
 580 585 590  
 Lys Asp Gln Ile Ser Val Leu Pro Asn Glu Gln Asp Leu Val Arg Glu  
 595 600 605  
 Glu Ala Gln Lys Met Ser Ser Leu Leu Pro Thr Met Trp Leu Gly Ala  
 610 615 620  
 Gln Asn Gly Cys Leu Tyr Val His Ser Ser Val Ala Gln Trp Arg Lys  
 625 630 635 640  
 Cys Leu His Ser Ile Lys Leu Lys Asp Ser Ile Leu Ser Ile Val His  
 645 650 655  
 Val Lys Gly Ile Val Leu Val Ala Leu Ala Asp Gly Thr Leu Ala Ile  
 660 665 670  
 Phe His Arg Gly Val Asp Gly Gln Trp Asp Leu Ser Asn Tyr His Leu  
 675 680 685  
 Leu Asp Leu Gly Arg Pro His His Ser Ile Arg Cys Met Thr Val Val  
 690 695 700  
 His Asp Lys Val Trp Cys Gly Tyr Arg Asn Lys Ile Tyr Val Val Gln  
 705 710 715 720  
 Pro Lys Ala Met Lys Ile Glu Lys Ser Phe Asp Ala His Pro Arg Lys  
 725 730 735  
 Glu Ser Gln Val Arg Gln Leu Ala Trp Val Gly Asp Gly Val Trp Val  
 740 745 750  
 Ser Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr Tyr  
 755 760 765  
 Gln His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val Ser Lys Met Leu  
 770 775 780  
 Gly Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Met  
 785 790 795 800  
 Val Ser Cys Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Ile Ile  
 805 810 815

Ser Ile Pro Leu Thr Glu Ser Lys Tyr Ile Phe Arg  
820 825

<210> 200  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 200  
tnagggttgc acttcttctt gcaaattcc

29

<210> 201  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 201  
cnaatatctg agtctgtcct gcgggactc

29

<210> 202  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 202  
cnggctctgt gatggctgaa tggaaagaa

29

<210> 203  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 203  
angagtccaa ttaaagaacg aaaagcggg 29

<210> 204  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 204  
cntcagcttg ggcaagagta aagagggca 29

<210> 205  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 205  
tnatttaaga tgctgtgtaa gcctctcgc 29

<210> 206  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 206  
tntctgtgtg cacagagctt tggagtggc 29

<210> 207  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 207  
gnttggattc tctggcagag tacacctgc 29

<210> 208  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 208  
gnaggcatat cttttacagg ttcagctcc 29

<210> 209  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 209  
cncagtgaga caggtagtag gagccagat 29

<210> 210  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 210  
angtaaattc cagccaggat gatggccgc 29



<210> 211  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 211  
tngagtgtgg aattgcgctt cttacctat

29

<210> 212  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 212  
gngtgaagtc ttcctgggaa ccataatct

29

<210> 213  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 213  
tnttcctga agagctggag aggtgctaa

29

<210> 214  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 214  
gntctaccat gtgaagaagg aacgcaaaa

29

<210> 215  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 215  
tnggcaaagc tgtgctgcag gatagagtg

29

<210> 216  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 216  
angtgaagga ctgtaagccc acacaagct

29

<210> 217  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 217  
tnatgacagc ccaggctgtg ttatctgca

29

<210> 218  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 218  
cngggccttc gttttcacta ccttcagaa

29

<210> 219  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 219  
tnaagacggt gactgagagg cagacaagg

29

<210> 220  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 220  
tncctagtcc ctttaggtag ctctgcaga

29

<210> 221  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 221  
gngcacgaga aagaaggcga ggatggcta

29

<210> 222  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 222  
tnggacactg tggattctga gtcttggtg

29

<210> 223  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 223  
ancaggaggc agtgggttct atagagtcc

29

<210> 224  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 224  
cncttggtg cctgtttctc aattgcaga

29

<210> 225  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 225  
cnctagctgt tcggctttac caaggagtt

29

<210> 226  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 226  
ancacgctct gacgaatgag caacctctc

29

<210> 227  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 227  
cnaacacaga ctggaagcct agagtcgct

29

<210> 228  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 228  
gnaaaccagg aatgtacac tgacacaat

29

<210> 229  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 229  
tnatcaatac tggtagacagt ctgctccaa 29

<210> 230  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 230  
gncataaccc ttgcacgaa gctgatctt 29

<210> 231  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 231  
anatttaagc atttaacgtg aaggatagg 29

<210> 232  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 232  
tnagagactg ggaaaccaac agccactgc 29

<210> 233  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 233  
anggagcaag ttcctgagag tatcctggt 29

<210> 234  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 234  
anggagcaag ttcctgagag tatcctggt 29

<210> 235  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 235  
gnatggaggg agagagaaca caaattaac 29

<210> 236  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 236  
gngacagtgt tgtgctgaag caggattcc 29

<210> 237  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 237  
cntctccaac ttccacaatt tgctcacta 29

<210> 238  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 238  
tnggaggaag agtggcagag gagcttata 29

<210> 239  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 239  
cngtggttttg ttcttaggaa ggtagaagc 29

<210> 240  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 240  
cngccagcca gcagcaaagc aaattaaga 29



<210> 241  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 241  
tngaggaaag aagggtggag gtctgcaca

29

<210> 242  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 242  
cggtgggatt tatttaacat gatcttggc

29

<210> 243  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 243  
ccaatgggta tgatgatggt tcttcct

27

<210> 244  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 244  
anggatgcca tccagatgag gccacagct

29

<210> 245  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 245

ancttcttct gcagctcatt caactcctg

29

<210> 246

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 246

gntcctccta gaccacaaag tagaaagca

29

<210> 247

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 247

gnctgacttt ctctccagtt tgtgaaatc

29

<210> 248

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 248

gngtgggggtg aaaagggaat gattagga

29

<210> 249

<211> 29

<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 249  
tnattcatgg gcagctcatt ggcgggctc

29

<210> 250  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 250  
cngctgagac tcacacactg aatttcctt

29

<210> 251  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 251  
cntcttggtc cggatgatgt ttttatcac

29

<210> 252  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 252

tntctcggtta tatggaggac gaatagact

29

<210> 253

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 253

ctctttatga gcatgatatg gcttcag

27

<210> 254

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 254

cntgctgccc gacttaaact gagaaccaa

29

<210> 255

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 255

gnngacaact cccatagttg aggtttgtc

29

<210> 256

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 256

tnggaagagt gacccagggg cccaaagca

29

<210> 257  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 257  
cnctgcaagc gagtgggtttt cagggctgt

29

<210> 258  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 258  
tngagccaag gagagagcag acaggctga

29

<210> 259  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 259  
ancccccaga agtacaagga catgccaag

29

<210> 260  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)

<223> biotinylated phosphoramidite residue

<400> 260  
cnatagcatc agcatcaaca tggtagcaa 29

<210> 261  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 261  
ctccattctc cttgactatc ttctccc 27

<210> 262  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 262  
tncttggtgc catcatgatt gtaggagc 29

<210> 263  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 263  
anaggctcct ccattcctac agccatctt 29

<210> 264  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 264  
cngtccaact gcttgtagggt tatagcaga 29

<210> 265  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 265  
tnctctactt cacccttttc ggtgcatcg 29

<210> 266  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 266  
tncataaaat gacccacac ctctactg 29

<210> 267  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 267  
gngaggtagc caggcatctc tgtgcattt 29

<210> 268  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 268  
ancacagcag gaggtgagga ggaggagat

29

<210> 269  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 269  
cnttgatctg agagcttttc accgtcaag

29

<210> 270  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 270  
anctgccaaag aagaggagag tggtaaatt

29

<210> 271  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 271  
angaaaaaga agtgatcatga tccagtaca

29

<210> 272  
<211> 29  
<212> DNA  
<213> Artificial Sequence



<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 272  
tnataacttgg acaggataga gcgaggttc 29

<210> 273  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 273  
cncgactgcc ttaaaatgta aacctggat 29

<210> 274  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 274  
tngcactggg aaagtgattg tgaggagta 29

<210> 275  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 275  
tngtgctgcc aaagaacagg agcctcaa 29

<210> 276  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 276  
ctgctgctca tttgttcaat aatgtcaac

29

<210> 277  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 277  
tngcactggt gtcacgacgg cttggtctc

29

<210> 278  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 278  
anaacagagc agtccagagg aagaacatc

29

<210> 279  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 279  
anatgaccag atcctctcag aagatttcc

29

<210> 280

<211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<220>  
 <221> misc\_feature  
 <222> (2)  
 <223> biotinylated phosphoramidite residue

<400> 280  
 tnccagtgc tgggcatgca tgaaggcta

29

<210> 281  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<220>  
 <221> misc\_feature  
 <222> (2)  
 <223> biotinylated phosphoramidite residue

<400> 281  
 ancagcaaac tcttcctttc gcttgctgc

29

<210> 282  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<220>  
 <221> misc\_feature  
 <222> (2)  
 <223> biotinylated phosphoramidite residue

<400> 282  
 tntttctcac aggtcagttc atccacttt

29

<210> 283  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<400> 283  
 Met Cys Arg Pro Phe Leu Ser Leu Leu Cys Ser Thr Lys Cys Phe  
 1 5 10 15

Leu Leu Cys Gly Leu Gly Gly Thr His Val Thr Phe Val Ser Cys Ser  
 20 25 30

Lys Ala Gly Ala Thr Pro Ser Ser Leu Phe Ser Thr Gln His Gln Ala

35

40

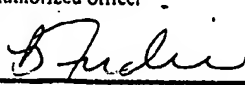
45

Leu Ser Arg His Pro Ile Asn His Cys  
50 55

Applicant's or agent's file reference 1290.1001010	International application No. <b>PCT/US 00/25135</b>
--	---

**INDICATIONS RELATING TO DEPOSITED MICROORGANISM  
OR OTHER BIOLOGICAL MATERIAL**

(PCT Rule 13bis)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on pages <u>333</u> , line <u>35</u> to <u>37</u>	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <b>AMERICAN TYPE CULTURE COLLECTION</b>	
Address of depositary institution (including postal code and country) <b>American Type Culture Collection (ATCC) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</b>	
Date of deposit <b>see Attachment A</b>	Accession Number <b>see Attachment A</b>
C. ADDITIONAL INDICATIONS (leave blank if not applicable)	
This information is continued on an additional sheet <input checked="" type="checkbox"/>	
In respect of those designations for which a European patent is sought, the Applicant(s) hereby informs the International Bureau that the Applicant wishes that, until the publication of the mention of the grant of a European patent or for 20 years from the date of filing if the application is refused or withdrawn or deemed to be withdrawn, the biological material deposited with the American Type Culture Collection under Accession No. <u>see Attachment A</u>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	
For receiving Office use only	For International Bureau use only
<input checked="" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer 	Authorized officer

**INDICATIONS RELATING TO A DEPOSITED MICROORGANISM**  
(Additional Sheet)

**C. ADDITIONAL INDICATIONS (Continued)**

shall be made available as provided in ~~Rule 28(3) EPC~~ only by the issue of a sample to an expert nominated by the requester (Rule 28(4) EPC).

In respect of the designation of Australia in the subject PCT application, and in accordance with Regulation 3.25(3) of the Australian Patents Regulations, the Applicant hereby gives notice that the furnishing of a sample of the biological material deposited with the American Type Culture Collection under Accession No. ~~Attachment A~~<sup>886</sup> shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention and who is nominated in a request for the furnishing of a sample.

In respect of the designation of Canada in the subject PCT application, the Applicant hereby informs the International Bureau that the Applicant wishes that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the biological material deposited with the American Type Culture Collection under Accession No. ~~Attachment A~~<sup>886</sup> and referred to in the application to an independent expert nominated by the Commissioner.

## Attachment A

-1-

Deposit of Clones

Clones AX65\_22, BD335\_14, BG241\_1, BL187\_4, BL249\_18, BO71\_1, BO365\_2, BV51\_1, BV140\_3, BV141\_2, CC194\_4, and DA136\_11 were deposited on October 3, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98196, from which each clone comprising a particular polynucleotide is obtainable.

Clones AR415\_4, AS63\_29, BG160\_1, BO432\_4, BO538\_2, BR595\_4, CI490\_2, CI522\_1, CN238\_1, CO390\_1, and AY304\_1 (an additional isolate of clone AY304\_14) were deposited on October 25, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98232, from which each clone comprising a particular polynucleotide is obtainable. Clone AY304\_14 was deposited on October 23, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98561.

Clones AJ20\_2, AR440\_1, AS164\_1, AX8\_1, BD176\_3, BD339\_1, BD427\_1, BL229\_22, BV123\_16, and CH377\_1 were deposited on November 15, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98261, from which each clone comprising a particular polynucleotide is obtainable.

Clones BD441\_1, BD441\_2, BG102\_3, BK158\_1, BP163\_1, BZ16\_3, CC182\_1, CG109\_1 and CJ397\_1 were deposited on November 20, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98264, from which each clone comprising a particular polynucleotide is obtainable.

Clones AM795\_4, AT340\_1, BG132\_1, BG219\_2, BG366\_2, BV172\_2, CC247\_10, CI480\_9, CO722\_1, and CT748\_2 were deposited on December 5, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98271, from which each clone comprising a particular polynucleotide is obtainable.

Clones AJ1\_1, AQ73\_3, BG142\_1, BV66\_1, BV291\_3, CK201\_1, CQ331\_2, CT550\_1, CT585\_1 and CT797\_3 were deposited on December 13, 1996 with the ATCC

## Attachment A

-2-

(American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98278, from which each clone comprising a particular polynucleotide is obtainable.

Clones CB107\_1, CG300\_3, CJ145\_1, CJ160\_11, CO20\_1, CO223\_1, CO310\_2, CP258\_3, CW1155\_3 and CZ247\_2 were deposited on December 17, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98279, from which each clone comprising a particular polynucleotide is obtainable. Clone CO223\_3 was deposited on January 9, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98291.

Clones AM666\_1, BN387\_3, BQ135\_2, CR678\_1, CW420\_2, CW795\_2, CW823\_3, DF989\_3, DL162\_2, DLi62\_i, and EC172\_i were deposited on January 10, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98292, from which each clone comprising a particular polynucleotide is obtainable.



## INTERNATIONAL SEARCH REPORT

International Application No

I US 00/25135

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/47 C12N1/21 C12N5/10 C12Q1/68  
A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, STRAND

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, L	WO 98 17687 A (GENETICS INST) 30 April 1998 (1998-04-30) the document throws doubt on the priority of the application abstract; claims 20-22 see SEQ ID NO: 8 and 9 (pp.73-77) page 18, line 30 -page 20, line 2 page 23, line 12 -page 24, line 14 page 31, line 12 -page 64, line 16 -----	1-11

☐ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&amp;" document member of the same patent family

Date of the actual completion of the international search

14 December 2000

Date of mailing of the international search report

3 0. 01. 01

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel (+31-70) 340-2040, Tx. 31 651 epo nl,  
Fax: (+31-70) 340-3016

Authorized officer

Oderwald, H

# INTERNATIONAL SEARCH REPORT

national application No.  
PCT/US 00/25135

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-11

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-11

An isolated polynucleotide comprising SEQ ID NO: 41 which encodes a protein of SEQ ID NO: 42 (BG160\_1). A host cell, a process for producing said protein, a protein produced by said process, a composition comprising said protein.

2. Claims: 12, 13

An isolated polynucleotide comprising SEQ ID NO: 129. A protein encoded by said polynucleotide having amino acid sequence SEQ ID NO: 130 (C0722\_1).

### Information on patent family members

F . US 00/25135

Form PCT/ISA/210 (patent family annex) (July 1992)